

Access DB#

12/951

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: David Fox Examiner #: 65401 Date: 5/12/04
Art Unit: 1638 Phone Number 30 20795 Serial Number: 09/701 023
Mail Box and Bldg/Room Location: REM 209 Results Format Preferred (circle): PAPER DISK E-MAIL
2C18

If more than one search is submitted, please prioritize searches in order of need. MEJ

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: 3/99

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

please search
renewed
DF SEQ ID NO: 2
stay
Thank you

RECEIVED
MAY 12 2004
(S10)

2NA-271

MEJ
5/13
14

STAFF USE ONLY

	Type of Search	Vendors and cost where applicable
Searcher: <u>Arnold</u>	NA Sequence (#) <u>1</u>	STN _____
Searcher Phone #: <u>2-2530</u>	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>5/13/04</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>5/17/04</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

nucleic - nucleic search, using sw model

m: May 16, 2004, 10:21:20 ; Search time 2969 Seconds
(without alignments)
3956.201 Million cell updates/sec

ct score: 271
nce: 1 gtagcatgatcttaacaa.....ctactcatgagctctcttca 271

ng table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

hed: 3470272 seqs, 21671516995 residues

number of hits satisfying chosen parameters: 6940544

um DB seq length: 0
num DB seq length: 2000000000

processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

ase :

GenEmbl.*
1: gb ba.*
2: gb htg.*
3: gb in.*
4: gb om.*
5: gb ov.*
6: gb pat.*
7: gb ph.*
8: gb pl.*
9: gb pr.*
10: gb ro.*
11: gb sts.*
12: gb sy.*
13: gb un.*
14: gb vi.*
15: em ba.*
16: em fun.*
17: em hum.*
18: em in.*
19: em mu.*
20: em or.*
21: em ov.*
22: em pat.*
23: em ph.*
24: em pl.*
25: em ro.*
26: em sts.*
27: em un.*
28: em vi.*
29: em htg hum.*
30: em htg inv.*
31: em htg other.*
32: em htg mus.*
33: em htg pln.*
34: em htg rod.*
35: em htg mam.*
36: em htg vrt.*
37: em sy.*
38: em htgo hum.*
39: em htgo mus.*
40: em htgo pln.*
41: em htgo other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	127.4	47.0	1133	8	AF146794	AF146794 Arabidops
2	127.4	47.0	1302	8	AF159255	AF159255 Arabidops
3	127.4	47.0	82381	8	ATP27G19	AL078467 Arabidops
4	127.4	47.0	83371	8	ATM4I22	AL030978 Arabidops
5	127.4	47.0	198372	8	ATCHRIV66	AL161566 Arabidops
6	45.2	16.7	357	11	BX664650	BX664650 Arabidops
7	43.6	16.1	414	8	AY027298	AY027298 Arabidops
8	41.2	15.2	208	12	AF519993	AF519993 Populus t
9	41.2	15.2	6875	12	AF433042	AF433042 Cloning v
10	41.2	15.2	6928	12	AF433043	AF433043 Cloning v
11	40.8	15.1	5772	8	AF355378	AF355378 Zea mays
12	40.6	15.0	8867	8	AY191010	AY191010 Zea mays
13	40.4	14.9	197	12	AF519994	AF519994 Populus t
14	40.4	14.9	407	12	AY201779	AY201779 Arabidops
15	40.4	14.9	716	12	AF519991	AF519991 Populus t
16	40.2	14.8	245	8	AY027084	AY027084 Arabidops
17	39.4	14.5	569	8	AY027300	AY027300 Arabidops
18	39.4	14.5	4810	8	MZEAC9WX	K01964 Maize trans
19	39.2	14.5	691	12	AY203557	AY203557 Arabidops
20	39.2	14.5	701	8	AY026975	AY026975 Arabidops
21	39	14.4	603	12	AF519992	AF519992 Populus t
22	39	14.4	658	12	AY200619	AY200619 Arabidops
23	39	14.4	835	12	AF519989	AF519989 Populus t
24	39	14.4	843	8	AY027085	AY027085 Arabidops
25	39	14.4	2115	8	AF332953	AF332953 Zea mays
26	39	14.4	3253	8	AF332952	AF332952 Zea mays
27	39	14.4	3897	8	AF332954	AF332954 Zea mays
28	39	14.4	4167	8	AF332955	AF332955 Zea mays
29	39	14.4	4565	6	AX235897	AX235897 Sequence
30	39	14.4	4565	8	ZMAC1	X05424 Maize trans
31	39	14.4	4565	8	ZMTAC	X01380 Zea mays tr
32	39	14.4	7635	12	AB055064	AB055064 Synthetic
33	39	14.4	28708	12	AY218787	AY218787 Cloning v
34	38.6	14.2	124	11	BX664506	BX664506 Arabidops
35	38.6	14.2	275	11	BX664695	BX664695 Arabidops
36	38.6	14.2	730	12	AY200988	AY200988 Arabidops
37	38.2	14.1	686	8	AY027284	AY027284 Arabidops
38	38	14.0	215	12	AY202414	AY202414 Arabidops
39	38	14.0	391	12	AF519997	AF519997 Populus t
40	38	14.0	587	12	AY203453	AY203453 Arabidops
41	38	14.0	799	8	AY027146	AY027146 Arabidops
42	37.8	13.9	189	12	AY201780	AY201780 Arabidops
43	37.8	13.9	240	12	AY201861	AY201861 Arabidops
44	37.8	13.9	351	12	AY201762	AY201762 Arabidops
45	37.8	13.9	352	12	AY202180	AY202180 Arabidops

ALIGNMENTS

RESULT 1
AF146794

LOCUS AF146794

DEFINITION Arabidopsis thaliana NOZZLE (NZ2)

ACCESSION AF146794

VERSION AF146794.1

KEYWORDS GI:5007008

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 1133)

AUTHORS Schiefthaler, U., Balasubramanian, S., Sieber, P., Chevalier, D., Wisman, E. and Schneitz, K.

1133 bp DNA linear PLN 29-SEP-1999
complete cds.

Too LATE

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1
 HORNS Bevan, M., Hilbert, H., Braun, M., Holzer, S., Brandt, A., Duesterhoeft, A., Bancroft, I., Mewes, H. W., Mayer, K. F. X., Lemcke, K., Mannhaupt, G. and Schueller, C. Unpublished

2 (bases 1 to 82381)

3 EU Arabidopsis sequencing project.

4 Direct Submission

5 Submitted (30-MAY-1999) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-8152 Martinsried, FRG, E-mail: schueller@mpi-biochem.mpg.de, mayer@mpi-biochem.mpg.de

6 Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk

7 Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>.

8 RES location/Qualifiers

9 1. 82381

10 /organism="Arabidopsis thaliana"

11 /mol_type="genomic DNA"

12 /variety="Columbia"

13 /db_xref="taxon:3702"

14 /chromosome="4"

15 misc_feature

16 1. 30951

17 /note="overlap to BAC M4122 ; please refer to this entry for analysis and annotation"

18 5126..5143

19 /note="there is a mismatch in this homopolimeric stretch to the overlapping BAC M4122: 18(F27G19) versus 17(M4122) A's; the genomic DNA clearly shows 18 A's"

20 31517..32602

21 /gene="F27G19.10"

22 complement(join(31517..31960,32044..32335,32394..32602))

23 /gene="F27G19.10"

24 complement(join(31517..31960,32044..32335,32394..32602))

25 /gene="F27G19.10"

26 /note="similarity to Arabidopsis thaliana nap gene, PID:e1234813"

27 contains EST gb:R83977"

28 /codon_start=1

29 /product="putative protein"

30 /protein_id="CAB43873.1"

31 /db_xref="GI:4972066"

32 /db_xref="SPTREMBL:Q9SZR8"

33 /translation="MGVREKDPQLAQLPPGFRFPTDELLVOVLCRKVAGYHFLQLVIGDILYKFDPLPSKQCTFTVGEYCNVGLKALFGEKEMVFFSPDRKYPNGSRPNRVAGSYWATGDKIITADGRVGIKKALVPYAGKAGTKTNWIMHEYRLIEHSRSHSSKLDLWVLCRIYKTKSGSORQAVTPVQACREHSTNGSSSSSSQDDVDSFPEIKQSFNLPMSLRITLNGFNFDWASLAGLNPPELAPTNGLPSYGGYDAFRAAEGBAESGHVNRQNSGLTQSGYSSSGFGVSGQTTEFRQ"

34 complement(31517..31960)

35 /gene="F27G19.10"

36 /number=1

37 complement(31961..32043)

38 /gene="F27G19.10"

39 /number=1

40 complement(32044..32335)

41 /gene="F27G19.10"

42 /number=2

43 complement(32336..32393)

44 /gene="F27G19.10"

45 /number=2

46 complement(32394..32602)

47 /gene="F27G19.10"

48 /number=3

49 34968..35014

50 /note="47bp at tandem repeat"

51 36023..38396

52 /gene="F27G19.20"

53 complement(join(36023..36688,36772..37103,37174..37326,

37369..38011,38273..38386))

/gene="F27G19.20"

complement(join(36023..36688,36772..37103,37174..37326,37369..38011,38273..38386))

/gene="F27G19.20"

/note="similarity to D.melanogaster P element CasPer-1 gene (white protein), PID:g87096"

contains ABC transporters family signature [VSGGRKRVSIGQEI], ATP/GTP-binding site motif A (P-loop) [GPSGSGKT] [ALTRIGKT]"

/codon_start=1

/product="putative protei"

/protein_id="CAB43874.1"

/db_xref="GI:4972067"

/db_xref="GOA:Q9SZR9"

/db_xref="SPTREMBL:Q9SZR9"

/translation="MDNQEVSMDEVPIAKTNDORSIPFSIFKKANNPVTLKFENLVYTVKLQSQCFCGKNDKTEERTILKGLTGIKPGCEILAMLGPSGSGKTSLTALGGRVYEGKLUITGNISYNNKPLSKAVKTTQTFVTDQDALYNLTVEITVFTALLRLNPSPKKOEIKAKAVTAEIGLDRCKDTIIGGFFLRVSGGRKRVSIGQEIILINPSLLFLDPEP TSGLDSTTAQRIYSIILWEIARGRTVVTTHQPSKGNPVYFGLGSNAMDYFASVGYSP LVERINPSDFLDIANGKPLLVISCPVSGSDSPPEAKMAALVAFYKTNLLDSVIN EVKQDDLCNKPRESRVANTYGDWPTTWQOFCVLLKRLKORRHDSFSGMKVAOIFIVSFCLLWQTKISRLQDQIGLLFFISSFWAFPLFOQIETFPQERAMLOKERS GMYRLSPYFLSRVVDGLPMELLIPTCLVTIYWMAGLNHNLANFFVTLVLLVHLVLS GGLGALGALVMDQKATTLIGSVIMLTFLLAGGYVQHVVFVSWIKYVSIYITTKL LILQVITANEIYPCGDNKLRCHVDFEGIKHIGFNSGLVSALALTAMLVVYRVIAVI ALTRIGKTKSG"

complement(36023..36688)

/gene="F27G19.20"

/number=1

complement(36689..36771)

/gene="F27G19.20"

/number=1

complement(36772..37103)

/gene="F27G19.20"

/number=2

complement(37104..37173)

/gene="F27G19.20"

/number=2

complement(37174..37326)

/gene="F27G19.20"

/number=3

complement(37327..37368)

/gene="F27G19.20"

/number=3

complement(37369..38011)

/gene="F27G19.20"

/number=4

complement(38012..38272)

/gene="F27G19.20"

/number=4

complement(38273..38386)

/gene="F27G19.20"

/number=5

42406..46325

/gene="F27G19.30"

join(42406..42464,42566..42742,42832..42953,43062..43114,43203..43246,43346..43498,43587..43813,43912..45359,45432..46325)

/gene="F27G19.30"

/note="contains EST gb:Z37620, Z37621"

/codon_start=1

/product="COPI1-interacting protein 7 (CIP7)"

/protein_id="CAB43875.1"

/db_xref="GI:4972068"

/db_xref="SPTREMBL:O80386"

/translation="MDPRTRLDYALFQITPTTRCDLVI FSGGENEKLASGIFQFPFVT HLKVSQDI SKGYSVTLRPSVGVGVPWFVKLQRFVRFTVTPTELSRVSYLEGIEQ IEDSIQANAAIAIEAECNEIGTWTQSKTALSKTKGTGDTGDTVEENSVKLQRLVE NRKAAALCKEQAMAYARALVGVFELDMDDLPSADAFGASRLREACVNFVLCRRKNE DRMWVDQITANQAFPRPELTFMGDSGIVLAGEENDLNATNVKGNNSMDSQGSFET QCEGRAQNAWEPNQFPQYMQNFQGHGYPFPYMPFGMQGQSPYFHGNQWPNVNGDVE


```

/product="putative protein"
/protein_id="CAA19715.1"
/db_xref="GI:3269282"
/db_xref="GOA:O81824"
/db_xref="SPTREMBL:O81824"
/translation="MGQPLHQIRSTYPSGROTESSNLGFLDPPRISSVWMLSTATH
MRLEFELQRQNVSRKDKTDAYLNDLKNICDQLQSGVSPTEKMK.FAALNGLGRXY
EPIKTTIENSMDQPGSLNDVYFKLGYDDRLQGYLEETITSPYAFNITTSDDSYR
NSYNGKDVTDQHNELWLPDAAHTVNDSPRSIQSQPYGHGDAIMVDDGNYLPITH
TSGNTLASSTGVLTDTVLVCPSTKSLGSLKLTQDPFCTVEPEYDGVNRVNDKATKK
LLNGSRDGLCLDKDQFOAFSPSTORGASDEWHRRGLGHPOILOPLERVHCDL
WGPTTITSVQGFYAYFIDHYSFESNIYPLKLSDFYNIFLAFHKLVENQLSKISV
PQDGGGEFVSKFLQHLQSHGIIQQOUCSPHTPOONGLABRKHRLVELGSLMDFQSH
VPHKFWAEFTANFLINLLPTSAKESISPYEKLYDKKPYDTSRFGSACFPFLRD
YAENKPNPCSLKCVFLNGEKYGRCLYPTPLRLYISRVIFDESVPFSPHYKHLH
POPTTELLAALWLRSSDPAESTSPSSRPLFTSADFPPLPQKRTPLLPVLPVSSV
SHASNITQOSPDPDSBRTTDPDSASIGDSHSSQAGSDSEETIQOASVAVHOTHAST
NVHPMTKVGISIKPMPRYVFLSHKVSYPKPVTAALKHGWTGAMTEIGNCSET
QWTSVAPYKSDMVLGSKWERTKLHAGDTLNLKARIKAVKGFQOEGSIDVLETISPV
VRTPTLRVLHLATLANWDIKQMDVQNAFLHGLDKETVYMQPAGFVDPKPDHVCIL
HKSITGLQSPRAWKDFSTFLLBFGFPCSKSDPSLFIYAHNNNLILLIYVDDMVIT
NSSOTISLALAKKPRMTDMGLHYFLGIQVORQOGLFMFSQOYAEOLLIAASM
EHCPLTPPLVQLDVRVPHQBELSDFTYFRSIAGKQYLTLPDLPQFANFVCOKM
HQPTISDFHLKRLIRLYIKGTTIWGISYSDRSPILLQAYSDDMGNCQKTRRSVGGLC
TFMGTNLVSWSSKGGPTVSRSTEAEBYKSLSDAASEILWSTLLRELRIPLPDPELF
CDNLASVLTANPAPFARTKHFDIDPHFRVRERKALVWVXHIPGSEQIADIFTKSLP
YEAFIHLRGLKGLVTLSPTPSLRGITINTIOVKPRQNFVVSNSAKKQACQCRPKPTT
QVQKRSASIKTEPSPVSPSYDKNRAGTTSNACTEKAFNLKLENRFITLDSPTA"
3583..3719
/gene="AT4927210"
/number=1
3720..3766
/gene="AT4927210"
/number=1
3767..4131
/gene="AT4927210"
/number=2
4132..4356
/gene="AT4927210"
/number=2
4357..4828
/gene="AT4927210"
/number=3
4829..4948
/gene="AT4927210"
/number=3
4949..7931
/gene="AT4927210"
/number=4
6801..8057
/gene="AT4927220"
/number=1
5962..12721
/gene="AT4927220"
/number=2
complement(9962..12721)
complement(9962..12721)
/gene="AT4927220"
/number=1
/notes="similarity to disease resistance protein RPS2,
Arabidopsis thaliana, PIR2:A54809
Contains ATP/GTP-binding site motif A (P-loop)
AA141-148;Prokaryotic membrane lipoprotein lipid
attachment site AA750-760;Eukaryotic thiol (cysteine)
proteases active sites AA449-459"
/codon_start=1
/product="putative protein"
/protein_id="CAA19716.1"
/db_xref="GI:3269283"
/db_xref="GOA:O81825"
/db_xref="SPTREMBL:O81825"
/translation="MFRSNARALRALKRNQVTKNEALRKSRIGQEKSLERKLRIW
LRKVENVPLGSLIILEKSSCAIMLKDQVLEKVRLEQOGLIKKIVSKSSRE
IVERVLGSPSPHQKTALEMLDKLCKLKKVQKLGWCGGVGKVTIVRTLNNDLLK
YAATQGFALVIVTYSKOFDLKRVQMDIAKRLGKFTREQMKQLGLTICERLIDLANF
LLILDVWHPIIDLQDGLPALERSKDSKVLTSSRRLEVCCQMNTNENIKVACLQKE

```

```

ANLFCNHNVEVANSNVKPIAKDVSGHCCGLPLAIITIGRTLGRKPQVFWKHTLML
LKBSAPSIDTEKIFGTLKLSYDFLODNMKSCFLFCALPPEDYSIKVSELMYVWABG
LIDGQHIEDMMNMGVTLVERLKDSCLLEDGSDCDVFKWHDVVDPAIFWFSQGEFP
HSLWAGRGLIEPFDQKPVSSVORVSMANKLERLPNNVIEGVTETLVLLQGNHVKVE
VPMGFLQAFNPLRILDSGVRITRFLPDSFNLSRLSLVLRNCKNLEPSSLVSLVKL
OFDLDLSEATRELPRGLEALSRLYICVSNYQLOISIPAGTILQLSSLEYLDWAGSAY
SMGIGKEEREGQATLDEVTCLPHQLAIKLLDVLSFVSFEDSLTKRLTKFOFLFS91
RSVSPGTGEGCLASDVNVVSNASIGWLLQHTVSLDINCEGLNGWPNLVTKSKSP
VAMKALSIHYFPLSLASGESQDLDFPNLEELSLDNVLESIGELNGFLGMLQKLIK
LLQVSCRCQRLRFLSDOILAGTLPNLOEIKVVSCLRELEFNFSFVDFCAESLLPK
LTVIKLKYLPQLRSLCNDRVLESLEHVESCESLKNLPFPVFGNTGMINEQAWWEYM
SRTLG"
complement(9962..12721)
/gene="AT4927220"
/number=1
13524..14334
/gene="AT4927230"
/number=1
complement(join(13524..13730,14146..14334))
/gene="AT4927230"
complement(join(13524..13730,14146..14334))
CDS
complement(join(13524..13730,14146..14334))
/notes="strong similarity to histone H2A.4, Triticum
aestivum, PIR2:S53521
Contains Histone H2A signature AA23-29
Contains EST gb:AL995882.1, T04821, T43418"
/codon_start=1
/product="histone H2A-like protein"
/protein_id="CAA19717.1"
/db_xref="GI:3269284"
/db_xref="GOA:O81826"
/db_xref="SPTREMBL:O81826"
/translation="MAGRGKGLSGAAKSTSRSSKAGLQFPVGRIRARFLKAGYKAR
VGAGAPVYLAALVLEYLAAYLEAGNAARDNKKTRIVPRHQLAVRNDSELSKLLGDV
TIANGVMPNHNLLLPKAGSSKPTTEED"
complement(13524..13730)
/gene="AT4927230"
/number=1
complement(13731..14145)
/gene="AT4927230"
/number=1
complement(14146..14334)
/gene="AT4927230"
/number=2
16169..17649
/gene="AT4927240"
/number=1
join(16169..16829,17015..17649)

```

Query Match	47.0%	Score 127.4	DB 8	Length 83371
Best Local Similarity	98.6%	Pred. No. 1e-31		
Matches 139	Conservative 0	Mismatches 1	Indels 1	Gaps 1
QY	132	GGGCTACAGGCTTCCCAAGCTCA-TCGGGAGACACAGGATCTATTGTGGTGGAGTCGGG	190	
Db	59138	GTGCTACAAGGCTTCCCAAGCTCACTCGGAGACACAGGATCTATTGTGGTGGAGTCGGG	59079	
QY	191	TCGGGTACAGGTTATGATCGACCGGTTATTTCTTCATCGGGTTTGTGTGAGACCTCTCC	250	
Db	59078	TCGGGTACAGGTTATGATCGACCGGTTATTTCTTCATCGGGTTTGTGTGAGACCTCTCC	59019	
QY	251	ACTACTCATGAGCTCTCTTCA	271	
Db	59018	ACTACTCATGAGCTCTCTTCA	58998	

RESULT 5
 ATCHRIV66/c
 LOCUS ATCHRIV66 198372 bp DNA linear PIN 16-MAR-2000
 DEFINITION Arabidopsis thaliana DNA chromosome 4, contig fragment No. 65.
 ACCESSION AL161566
 VERSION AL161566.2 GI:7269538
 KEYWORDS Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 ORGANISM Arabidopsis thaliana

REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid1; brassicales; Brassicaceae; Arabidopsids.	exon	/number=2 complement(7485..7689) /gene="AT4g26860"
AUTHORS	1 (bases 1 to 84117) Lecharny,A., Chefodor,F., Krivitzky,M., Kreis,M., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.	intron	/number=3 complement(7690..7763) /gene="AT4g26860"
JOURNAL	Unpublished	exon	/number=3 complement(7764..7851) /gene="AT4g26860"
REFERENCE	2 (bases 83512 to 129491) Robben,J., Grymonprez,B., Volckaert,G., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.	intron	/number=4 complement(7852..7955) /gene="AT4g26860"
AUTHORS	3 (bases 127847 to 198372) Reichert,B.J., Barel,E., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.	exon	/number=4 complement(7956..8002) /gene="AT4g26860"
JOURNAL	Unpublished	intron	/number=5 complement(8003..8080) /gene="AT4g26860"
AUTHORS	4 (bases 185358 to 185634) Volckaert,G., Grymonprez,B., Voet,M., Robben,J., Mewes,H.W., Lemcke,K. and Mayer,K.F.X.	exon	/number=5 complement(8081..8147) /gene="AT4g26860"
JOURNAL	Unpublished	intron	/number=6 complement(8148..8326) /gene="AT4g26860"
REFERENCE	5 (bases 1 to 198372) EU Arabidopsis sequencing, project.	exon	/number=6 complement(8327..8548) /gene="AT4g26860"
AUTHORS	Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk	gene	/number=7 9236..11474 /gene="AT4g26870"
COMMENT	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/chal/ this fragment has an overlap with ATCHRIV67 at the 3' end.	CDS	Join(9236..9715,9783..9893,9996..10079,10191..10481,10555..10665,10874..11069,11156..11270,11348..11474) /gene="AT4g26870"
FEATURES	Location/Qualifiers		/note="similarity to aspartate-tRNA ligase (EC 6.1.1.12) -Methanobacterium thermoautotrophicum, GB:A5000809 Contains Aminoacyl-transfer RNA synthetases class-II signatures AA293-311;Aminoacyl-transfer RNA synthetases class-II signatures AA473-482 contains EST gb:234062, AA720362"
source	1..198372 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /variety="Columbia" /db_xref="taxon:3702" /chromosome="4"		/codon_start=1 /product="putative aspartate-tRNA ligase" /protein_id="CAB79542.1" /db_xref="GI:7269540" /db_xref="GOA:Q9S227" /db_xref="SPTREMBL:Q9S227"
gene	7146..8548 /gene="AT4g26860"		/translation="MVGSEVLEECGKISKESKKRAAKLEKLRKQREATSSLS LEEDESSSNYGDTTNELOSAGEKELDVSNLVEIIVGSEVSRGRHLKRLVGT KLFLVRESGFTVQVVEETRVGAMIKFVKQSRSEVLIIVSVHPKPLTGTTQ VEIHRWYCLSRPLNPLVVEDAARSDDIEKSGKDTLRNNRVLDIRTPANQAIER IQCOVQIAPREYLOSKGLEIHTPKLIAGSSEGSVAERLDYKQAPACQSPQHLKQ MAICDMRRVFEVGVFRAEDSFTHRHLCEVGLDVEIMHYSEIMDLVGELEFFI FTKIERCPKELSVRKQYFPQSLKEAGEVDPLGLDNTSEKLGQVLEKRECEFI MLHYPGAVRFPYTPYNDNSDFVIRGEEIMSGAQRHDPBLLKRECEGI DKVTITSYIDAFRYGAPGHGFGVGLERVVLLCALNNIRKTSLEPRDSQRLTP"
gene	complement(join(7146..7223,7356..7437,7485..7689,7764..7851,7956..8002,8081..8147,8327..8548)) /gene="AT4g26860"	exon	/number=1 /gene="AT4g26870"
CDS	complement(join(7146..7223,7356..7437,7485..7689,7764..7851,7956..8002,8081..8147,8327..8548)) /genes="AT4g26860" /note="strong similarity to proline synthetase associated - Homo sapiens, PID:di037830 Contains Uncharacterized protein family UPF0001 signature AA81-95 contains EST gb:AI995798.1, N97000, T76579"	intron	/number=1 9716..9782 /gene="AT4g26870"
		exon	/number=1 9783..9893 /gene="AT4g26870"
exon	complement(7146..7223) /gene="AT4g26860"	intron	/number=2 9894..9995 /gene="AT4g26870"
intron	complement(7224..7355) /gene="AT4g26860"	exon	/number=2 9996..10079 /gene="AT4g26870"
exon	complement(7356..7437) /gene="AT4g26860"	intron	/number=3 10080..10190 /gene="AT4g26870"
intron	complement(7438..7484) /gene="AT4g26860"	exon	/number=3 10191..10481


```
/gene="AT4g26870"
/number=4
10482..10554
/gene="AT4g26870"
/number=4
10555..10665
/gene="AT4g26870"
/number=5
10666..10873
/gene="AT4g26870"
/number=5
10874..11069
/gene="AT4g26870"
/number=6
11070..11155
/gene="AT4g26870"
/number=6
11156..11270
/gene="AT4g26870"
/number=7
11271..11347
/gene="AT4g26870"
/number=7
11348..11474
/gene="AT4g26870"
/number=8
12120..12578
/gene="AT4g26880"
complement(12120..12578)
/gene="AT4g26880"
complement(12120..12578)
/gene="AT4g26880"
/number=1
15927..17261
/gene="AT4g26890"

3ry Match 47.0%; Score 127.4; DB 8; Length 198372;
3t Local Similarity 98.6%; Pred. No. 1:1e-31;
:ches 139; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

132 GGGCTACAAGGCTTCCCAAGCTCA-TCGGGAGCAACAGGATCTATTGTGGTGGAGTCGGG 190
186984 GTGCTACAAGGCTTCCCAAGCTCATCTCGGAGCAACAGATCTATTGTGGTGGAGTCGGG 186925
191 TCGGGTCAGGTTATGATGACCCGGTTATTTTCCATCGGGTTTTTGTGAGACCTCTCC 250
186924 TCGGGTCAGGTTATGATGACCCGGTTATTTTCCATCGGGTTTTTGTGAGACCTCTCC 186865
251 ACTACTCATGAGCTCTCTTCA 271
186864 ACTACTCATGAGCTCTCTTCA 186844

LT 6
4650/c
S BX664650 357 bp DNA linear STS 14-OCT-2003
NTION Arabidopsis thaliana transposon insertion STS AT_3.3335, sequence
tagged site.
SSION BX664650
ION BX664650.1 GI:37665142
DRDS: STS; STS, sequence tagged site.
```

```
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1
REFERENCE Clarke,J.H., Bowles,B., Carter,J., Hart,D., McCullagh,B., Walsh,S.,
AUTHORS Langham,S., LeGrys,C., Jones,J.D.G. and Bevan,M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 357)
AUTHORS Clarke,J.H.
TITLE Direct Submission
JOURNAL Submitted (14-OCT-2003) Clarke J.H., John Innes Centre, Colney
Lane, Norwich, NR4 7UO, UK
COMMENT AT denotes an activation tag dissociation transposon within a
single line, ET an enhancer trap dissociation transposon, GT a gene
trap dissociation transposon, MT a mis-expression enhancer trap
dissociation transposon, SM a defective suppressor mutator
transposon. _3 denotes a sequence derived from the 3'end of the
transposon, _5 denotes a sequence derived from the 5'end of the
transposon BBSRC GARNET, ATIS project
On-line seed stock requests: http://nasc.nott.ac.uk/ NASC stock
code: NU101026.
FEATURES Location/Qualifiers
source 1..357
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="Landsberg erecta NASC stock code NW20"
/cultivar="Tn13xTn25"
/db_xref="taxon:3702"
/clone="AC008148"
1..357
/standard_name="AT_3.3335"
ORIGIN
Query Match 16.7%; Score 45.2; DB 11; Length 357;
Best Local Similarity 86.2%; Pred. No. 0.0007;
Matches 50; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Qy 43 GTACACCGGGTGTCTCTACAGGATGAACGCGTGAACGGTCGGTAAATATC 100
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 68 GTAGACTTGGGTACTTTTATAGGATGAACGCGTGAACGGTCGGTAAATATC 11
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
AY027298/c 414 bp DNA linear PLN 27-MAR-2001
LOCUS Arabidopsis thaliana sequence flanking 3' end of Ds-Genetrapp
DEFINITION insertion from line GT6240.
ACCESSION AY027298
VERSION AY027298.1 GI:13449835
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 414)
May,B.P., Simorowski,J., Arroyo,J.M., Shen,R., Healy,J., Reiner,A.,
McCombie,W.R. and Martienssen,R.A.
Genomic distribution of Ds enhancer trap and gene trap insertions
in transgenic Arabidopsis thaliana
Unpublished
2 (bases 1 to 414)
May,B.P., Simorowski,J., Arroyo,J.M., Shen,R., Healy,J., Reiner,A.,
McCombie,W.R. and Martienssen,R.A.
Direct Submission
JOURNAL Submitted (07-FEB-2001) Cold Spring Harbor Laboratory, 1 Bungtown
REFERENCE Road, Cold Spring Harbor, NY 11724, USA
AUTHORS Location/Qualifiers
1..414
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
```



```
/db_xref="GI:16903091"
/translation="MVRPVTPTREIKKLDGLWAFSLDRENCIGIDRWESALQESRA
IAPVGFNDQADADIRNAGNVYQREVPKMGAGQRIIVLRFDAVTHYKVVNNQ
EVMHOGGTPPEADVPYVIAKGSVRIIVCVNNELNMTIPPGWITIDENGKKQSY
FHDFVAGIHSRVMYLTNTTVDITVTHVAQDNHASVDQVAVGVSVAV
ADQVATCGTSGTQVNVPHLMQEGSYLYELCVTAKSOTEDLYELRVGHSVAV
KGSQFLNHKPPFTQGRHEDADLRGKDFNVLVHDMWIGANSYRTSHYPA
EEMLWADGHIIVDITAAVGNLIGIGFEAGNPKELYSEAVNGETQQAHQAI
KELIARDKHPSVVMMSIANEPTRPGQAREYFAPLAETKLDTPRPTICVNMFC
AHTDTISDLFDVLCNRYGYVQSGDLETAELKELAMOEKHLQPIIITEYVD
TLAGLSMYTDMWSEETOCALMDMYHRVDRVSAVGEQVWNFADPATSQILRVGN
KKGIFTRDRPKSAAFLLQKRWGMNFGKPPQGGKQ"
complement(6381..6414)
/notes="CaMV 35S promoter -46 region"

N

misc_feature
15.2%; Score 41.2; DB 12; Length 6875;
Best Local Similarity 74.3%; Pred. No. 0.019;
Matches 52; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

try:Match
118 CCTACTTTCA 127
6807 TCATATTAA 6798

AF433043 6928 bp DNA circular SYN 11-NOV-2001
AF433043
Cloning vector pWS32, complete sequence.
AF433043
AF433043.1 GI:16903092
ORF1
ORF2
ORF3
ORF4
ORF5
ORF6
ORF7
ORF8
ORF9
ORF10
ORF11
ORF12
ORF13
ORF14
ORF15
ORF16
ORF17
ORF18
ORF19
ORF20
ORF21
ORF22
ORF23
ORF24
ORF25
ORF26
ORF27
ORF28
ORF29
ORF30
ORF31
ORF32
ORF33
ORF34
ORF35
ORF36
ORF37
ORF38
ORF39
ORF40
ORF41
ORF42
ORF43
ORF44
ORF45
ORF46
ORF47
ORF48
ORF49
ORF50
ORF51
ORF52
ORF53
ORF54
ORF55
ORF56
ORF57
ORF58
ORF59
ORF60
ORF61
ORF62
ORF63
ORF64
ORF65
ORF66
ORF67
ORF68
ORF69
ORF70
ORF71
ORF72
ORF73
ORF74
ORF75
ORF76
ORF77
ORF78
ORF79
ORF80
ORF81
ORF82
ORF83
ORF84
ORF85
ORF86
ORF87
ORF88
ORF89
ORF90
ORF91
ORF92
ORF93
ORF94
ORF95
ORF96
ORF97
ORF98
ORF99
ORF100
ORF101
ORF102
ORF103
ORF104
ORF105
ORF106
ORF107
ORF108
ORF109
ORF110
ORF111
ORF112
ORF113
ORF114
ORF115
ORF116
ORF117
ORF118
ORF119
ORF120
ORF121
ORF122
ORF123
ORF124
ORF125
ORF126
ORF127
ORF128
ORF129
ORF130
ORF131
ORF132
ORF133
ORF134
ORF135
ORF136
ORF137
ORF138
ORF139
ORF140
ORF141
ORF142
ORF143
ORF144
ORF145
ORF146
ORF147
ORF148
ORF149
ORF150
ORF151
ORF152
ORF153
ORF154
ORF155
ORF156
ORF157
ORF158
ORF159
ORF160
ORF161
ORF162
ORF163
ORF164
ORF165
ORF166
ORF167
ORF168
ORF169
ORF170
ORF171
ORF172
ORF173
ORF174
ORF175
ORF176
ORF177
ORF178
ORF179
ORF180
ORF181
ORF182
ORF183
ORF184
ORF185
ORF186
ORF187
ORF188
ORF189
ORF190
ORF191
ORF192
ORF193
ORF194
ORF195
ORF196
ORF197
ORF198
ORF199
ORF200
ORF201
ORF202
ORF203
ORF204
ORF205
ORF206
ORF207
ORF208
ORF209
ORF210
ORF211
ORF212
ORF213
ORF214
ORF215
ORF216
ORF217
ORF218
ORF219
ORF220
ORF221
ORF222
ORF223
ORF224
ORF225
ORF226
ORF227
ORF228
ORF229
ORF230
ORF231
ORF232
ORF233
ORF234
ORF235
ORF236
ORF237
ORF238
ORF239
ORF240
ORF241
ORF242
ORF243
ORF244
ORF245
ORF246
ORF247
ORF248
ORF249
ORF250
ORF251
ORF252
ORF253
ORF254
ORF255
ORF256
ORF257
ORF258
ORF259
ORF260
ORF261
ORF262
ORF263
ORF264
ORF265
ORF266
ORF267
ORF268
ORF269
ORF270
ORF271
ORF272
ORF273
ORF274
ORF275
ORF276
ORF277
ORF278
ORF279
ORF280
ORF281
ORF282
ORF283
ORF284
ORF285
ORF286
ORF287
ORF288
ORF289
ORF290
ORF291
ORF292
ORF293
ORF294
ORF295
ORF296
ORF297
ORF298
ORF299
ORF300
ORF301
ORF302
ORF303
ORF304
ORF305
ORF306
ORF307
ORF308
ORF309
ORF310
ORF311
ORF312
ORF313
ORF314
ORF315
ORF316
ORF317
ORF318
ORF319
ORF320
ORF321
ORF322
ORF323
ORF324
ORF325
ORF326
ORF327
ORF328
ORF329
ORF330
ORF331
ORF332
ORF333
ORF334
ORF335
ORF336
ORF337
ORF338
ORF339
ORF340
ORF341
ORF342
ORF343
ORF344
ORF345
ORF346
ORF347
ORF348
ORF349
ORF350
ORF351
ORF352
ORF353
ORF354
ORF355
ORF356
ORF357
ORF358
ORF359
ORF360
ORF361
ORF362
ORF363
ORF364
ORF365
ORF366
ORF367
ORF368
ORF369
ORF370
ORF371
ORF372
ORF373
ORF374
ORF375
ORF376
ORF377
ORF378
ORF379
ORF380
ORF381
ORF382
ORF383
ORF384
ORF385
ORF386
ORF387
ORF388
ORF389
ORF390
ORF391
ORF392
ORF393
ORF394
ORF395
ORF396
ORF397
ORF398
ORF399
ORF400
ORF401
ORF402
ORF403
ORF404
ORF405
ORF406
ORF407
ORF408
ORF409
ORF410
ORF411
ORF412
ORF413
ORF414
ORF415
ORF416
ORF417
ORF418
ORF419
ORF420
ORF421
ORF422
ORF423
ORF424
ORF425
ORF426
ORF427
ORF428
ORF429
ORF430
ORF431
ORF432
ORF433
ORF434
ORF435
ORF436
ORF437
ORF438
ORF439
ORF440
ORF441
ORF442
ORF443
ORF444
ORF445
ORF446
ORF447
ORF448
ORF449
ORF450
ORF451
ORF452
ORF453
ORF454
ORF455
ORF456
ORF457
ORF458
ORF459
ORF460
ORF461
ORF462
ORF463
ORF464
ORF465
ORF466
ORF467
ORF468
ORF469
ORF470
ORF471
ORF472
ORF473
ORF474
ORF475
ORF476
ORF477
ORF478
ORF479
ORF480
ORF481
ORF482
ORF483
ORF484
ORF485
ORF486
ORF487
ORF488
ORF489
ORF490
ORF491
ORF492
ORF493
ORF494
ORF495
ORF496
ORF497
ORF498
ORF499
ORF500
ORF501
ORF502
ORF503
ORF504
ORF505
ORF506
ORF507
ORF508
ORF509
ORF510
ORF511
ORF512
ORF513
ORF514
ORF515
ORF516
ORF517
ORF518
ORF519
ORF520
ORF521
ORF522
ORF523
ORF524
ORF525
ORF526
ORF527
ORF528
ORF529
ORF530
ORF531
ORF532
ORF533
ORF534
ORF535
ORF536
ORF537
ORF538
ORF539
ORF540
ORF541
ORF542
ORF543
ORF544
ORF545
ORF546
ORF547
ORF548
ORF549
ORF550
ORF551
ORF552
ORF553
ORF554
ORF555
ORF556
ORF557
ORF558
ORF559
ORF560
ORF561
ORF562
ORF563
ORF564
ORF565
ORF566
ORF567
ORF568
ORF569
ORF570
ORF571
ORF572
ORF573
ORF574
ORF575
ORF576
ORF577
ORF578
ORF579
ORF580
ORF581
ORF582
ORF583
ORF584
ORF585
ORF586
ORF587
ORF588
ORF589
ORF590
ORF591
ORF592
ORF593
ORF594
ORF595
ORF596
ORF597
ORF598
ORF599
ORF600
ORF601
ORF602
ORF603
ORF604
ORF605
ORF606
ORF607
ORF608
ORF609
ORF610
ORF611
ORF612
ORF613
ORF614
ORF615
ORF616
ORF617
ORF618
ORF619
ORF620
ORF621
ORF622
ORF623
ORF624
ORF625
ORF626
ORF627
ORF628
ORF629
ORF630
ORF631
ORF632
ORF633
ORF634
ORF635
ORF636
ORF637
ORF638
ORF639
ORF640
ORF641
ORF642
ORF643
ORF644
ORF645
ORF646
ORF647
ORF648
ORF649
ORF650
ORF651
ORF652
ORF653
ORF654
ORF655
ORF656
ORF657
ORF658
ORF659
ORF660
ORF661
ORF662
ORF663
ORF664
ORF665
ORF666
ORF667
ORF668
ORF669
ORF670
ORF671
ORF672
ORF673
ORF674
ORF675
ORF676
ORF677
ORF678
ORF679
ORF680
ORF681
ORF682
ORF683
ORF684
ORF685
ORF686
ORF687
ORF688
ORF689
ORF690
ORF691
ORF692
ORF693
ORF694
ORF695
ORF696
ORF697
ORF698
ORF699
ORF700
ORF701
ORF702
ORF703
ORF704
ORF705
ORF706
ORF707
ORF708
ORF709
ORF710
ORF711
ORF712
ORF713
ORF714
ORF715
ORF716
ORF717
ORF718
ORF719
ORF720
ORF721
ORF722
ORF723
ORF724
ORF725
ORF726
ORF727
ORF728
ORF729
ORF730
ORF731
ORF732
ORF733
ORF734
ORF735
ORF736
ORF737
ORF738
ORF739
ORF740
ORF741
ORF742
ORF743
ORF744
ORF745
ORF746
ORF747
ORF748
ORF749
ORF750
ORF751
ORF752
ORF753
ORF754
ORF755
ORF756
ORF757
ORF758
ORF759
ORF760
ORF761
ORF762
ORF763
ORF764
ORF765
ORF766
ORF767
ORF768
ORF769
ORF770
ORF771
ORF772
ORF773
ORF774
ORF775
ORF776
ORF777
ORF778
ORF779
ORF780
ORF781
ORF782
ORF783
ORF784
ORF785
ORF786
ORF787
ORF788
ORF789
ORF790
ORF791
ORF792
ORF793
ORF794
ORF795
ORF796
ORF797
ORF798
ORF799
ORF800
ORF801
ORF802
ORF803
ORF804
ORF805
ORF806
ORF807
ORF808
ORF809
ORF810
ORF811
ORF812
ORF813
ORF814
ORF815
ORF816
ORF817
ORF818
ORF819
ORF820
ORF821
ORF822
ORF823
ORF824
ORF825
ORF826
ORF827
ORF828
ORF829
ORF830
ORF831
ORF832
ORF833
ORF834
ORF835
ORF836
ORF837
ORF838
ORF839
ORF840
ORF841
ORF842
ORF843
ORF844
ORF845
ORF846
ORF847
ORF848
ORF849
ORF850
ORF851
ORF852
ORF853
ORF854
ORF855
ORF856
ORF857
ORF858
ORF859
ORF860
ORF861
ORF862
ORF863
ORF864
ORF865
ORF866
ORF867
ORF868
ORF869
ORF870
ORF871
ORF872
ORF873
ORF874
ORF875
ORF876
ORF877
ORF878
ORF879
ORF880
ORF881
ORF882
ORF883
ORF884
ORF885
ORF886
ORF887
ORF888
ORF889
ORF890
ORF891
ORF892
ORF893
ORF894
ORF895
ORF896
ORF897
ORF898
ORF899
ORF900
ORF901
ORF902
ORF903
ORF904
ORF905
ORF906
ORF907
ORF908
ORF909
ORF910
ORF911
ORF912
ORF913
ORF914
ORF915
ORF916
ORF917
ORF918
ORF919
ORF920
ORF921
ORF922
ORF923
ORF924
ORF925
ORF926
ORF927
ORF928
ORF929
ORF930
ORF931
ORF932
ORF933
ORF934
ORF935
ORF936
ORF937
ORF938
ORF939
ORF940
ORF941
ORF942
ORF943
ORF944
ORF945
ORF946
ORF947
ORF948
ORF949
ORF950
ORF951
ORF952
ORF953
ORF954
ORF955
ORF956
ORF957
ORF958
ORF959
ORF960
ORF961
ORF962
ORF963
ORF964
ORF965
ORF966
ORF967
ORF968
ORF969
ORF970
ORF971
ORF972
ORF973
ORF974
ORF975
ORF976
ORF977
ORF978
ORF979
ORF980
ORF981
ORF982
ORF983
ORF984
ORF985
ORF986
ORF987
ORF988
ORF989
ORF990
ORF991
ORF992
ORF993
ORF994
ORF995
ORF996
ORF997
ORF998
ORF999
ORF1000
ORF1001
ORF1002
ORF1003
ORF1004
ORF1005
ORF1006
ORF1007
ORF1008
ORF1009
ORF1010
ORF1011
ORF1012
ORF1013
ORF1014
ORF1015
ORF1016
ORF1017
ORF1018
ORF1019
ORF1020
ORF1021
ORF1022
ORF1023
ORF1024
ORF1025
ORF1026
ORF1027
ORF1028
ORF1029
ORF1030
ORF1031
ORF1032
ORF1033
ORF1034
ORF1035
ORF1036
ORF1037
ORF1038
ORF1039
ORF1040
ORF1041
ORF1042
ORF1043
ORF1044
ORF1045
ORF1046
ORF1047
ORF1048
ORF1049
ORF1050
ORF1051
ORF1052
ORF1053
ORF1054
ORF1055
ORF1056
ORF1057
ORF1058
ORF1059
ORF1060
ORF1061
ORF1062
ORF1063
ORF1064
ORF1065
ORF1066
ORF1067
ORF1068
ORF1069
ORF1070
ORF1071
ORF1072
ORF1073
ORF1074
ORF1075
ORF1076
ORF1077
ORF1078
ORF1079
ORF1080
ORF1081
ORF1082
ORF1083
ORF1084
ORF1085
ORF1086
ORF1087
ORF1088
ORF1089
ORF1090
ORF1091
ORF1092
ORF1093
ORF1094
ORF1095
ORF1096
ORF1097
ORF1098
ORF1099
ORF1100
ORF1101
ORF1102
ORF1103
ORF1104
ORF1105
ORF1106
ORF1107
ORF1108
ORF1109
ORF1110
ORF1111
ORF1112
ORF1113
ORF1114
ORF1115
ORF1116
ORF1117
ORF1118
ORF1119
ORF1120
ORF1121
ORF1122
ORF1123
ORF1124
ORF1125
ORF1126
ORF1127
ORF1128
ORF1129
ORF1130
ORF1131
ORF1132
ORF1133
ORF1134
ORF1135
ORF1136
ORF1137
ORF1138
ORF1139
ORF1140
ORF1141
ORF1142
ORF1143
ORF1144
ORF1145
ORF1146
ORF1147
ORF1148
ORF1149
ORF1150
ORF1151
ORF1152
ORF1153
ORF1154
ORF1155
ORF1156
ORF1157
ORF1158
ORF1159
ORF1160
ORF1161
ORF1162
ORF1163
ORF1164
ORF1165
ORF1166
ORF1167
ORF1168
ORF1169
ORF1170
ORF1171
ORF1172
ORF1173
ORF1174
ORF1175
ORF1176
ORF1177
ORF1178
ORF1179
ORF1180
ORF1181
ORF1182
ORF1183
ORF1184
ORF1185
ORF1186
ORF1187
ORF1188
ORF1189
ORF1190
ORF1191
ORF1192
ORF1193
ORF1194
ORF1195
ORF1196
ORF1197
ORF1198
ORF1199
ORF1200
ORF1201
ORF1202
ORF1203
ORF1204
ORF1205
ORF1206
ORF1207
ORF1208
ORF1209
ORF1210
ORF1211
ORF1212
ORF1213
ORF1214
ORF1215
ORF1216
ORF1217
ORF1218
ORF1219
ORF1220
ORF1221
ORF1222
ORF1223
ORF1224
ORF1225
ORF1226
ORF1227
ORF1228
ORF1229
ORF1230
ORF1231
ORF1232
ORF1233
ORF1234
ORF1235
ORF1236
ORF1237
ORF1238
ORF1239
ORF1240
ORF1241
ORF1242
ORF1243
ORF1244
ORF1245
ORF1246
ORF1247
ORF1248
ORF1249
ORF1250
ORF1251
ORF1252
ORF1253
ORF1254
ORF1255
ORF1256
ORF1257
ORF1258
ORF1259
ORF1260
ORF1261
ORF1262
ORF1263
ORF1264
ORF1265
ORF1266
ORF1267
ORF1268
ORF1269
ORF1270
ORF1271
ORF1272
ORF1273
ORF1274
ORF1275
ORF1276
ORF1277
ORF1278
ORF1279
ORF1280
ORF1281
ORF1282
ORF1283
ORF1284
ORF1285
ORF1286
ORF1287
ORF1288
ORF1289
ORF1290
ORF1291
ORF1292
ORF1293
ORF1294
ORF1295
ORF1296
ORF1297
ORF1298
ORF1299
ORF1300
ORF1301
ORF1302
ORF1303
ORF1304
ORF1305
ORF1306
ORF1307
ORF1308
ORF1309
ORF1310
ORF1311
ORF1312
ORF1313
ORF1314
ORF1315
ORF1316
ORF1317
ORF1318
ORF1319
ORF1320
ORF1321
ORF1322
ORF1323
ORF1324
ORF1325
ORF1326
ORF1327
ORF1328
ORF1329
ORF1330
ORF1331
ORF1332
ORF1333
ORF1334
ORF1335
ORF1336
ORF1337
ORF1338
ORF1339
ORF1340
ORF1341
ORF1342
ORF1343
ORF1344
ORF1345
ORF1346
ORF1347
ORF1348
ORF1349
ORF1350
ORF1351
ORF1352
ORF1353
ORF1354
ORF1355
ORF1356
ORF1357
ORF1358
ORF1359
ORF1360
ORF1361
ORF1362
ORF1363
ORF1364
ORF1365
ORF1366
ORF1367
ORF1368
ORF1369
ORF1370
ORF1371
ORF1372
ORF1373
ORF1374
ORF1375
ORF1376
ORF1377
ORF1378
ORF1379
ORF1380
ORF1381
ORF1382
ORF1383
ORF1384
ORF1385
ORF1386
ORF1387
ORF1388
ORF1389
ORF1390
ORF1391
ORF1392
ORF1393
ORF1394
ORF1395
ORF1396
ORF1397
ORF1398
ORF1399
ORF1400
ORF1401
ORF1402
ORF1403
ORF1404
ORF1405
ORF1406
ORF1407
ORF1408
ORF1409
ORF1410
ORF1411
ORF1412
ORF1413
ORF1414
ORF1415
ORF1416
ORF1417
ORF1418
ORF1419
ORF1420
ORF1421
ORF1422
ORF1423
ORF1424
ORF1425
ORF1426
ORF1427
ORF1428
ORF1429
ORF1430
ORF1431
ORF1432
ORF1433
ORF1434
ORF1435
ORF1436
ORF1437
ORF1438
ORF1439
ORF1440
ORF1441
ORF1442
ORF1443
ORF1444
ORF1445
ORF1446
ORF1447
ORF1448
ORF1449
ORF1450
ORF1451
ORF1452
ORF1453
ORF1454
ORF1455
ORF1456
ORF1457
ORF1458
ORF1459
ORF1460
ORF1461
ORF1462
ORF1463
ORF1464
ORF1465
ORF1466
ORF1467
ORF1468
ORF1469
ORF1470
ORF1471
ORF1472
ORF1473
ORF1474
ORF1475
ORF1476
ORF1477
ORF1478
ORF1479
ORF1480
ORF1481
ORF1482
ORF1483
ORF1484
ORF1485
ORF1486
ORF1487
ORF1488
ORF1489
ORF1490
ORF1491
ORF1492
ORF1493
ORF1494
ORF1495
ORF1496
ORF1497
ORF1498
ORF1499
ORF1500
ORF1501
ORF1502
ORF1503
ORF1504
ORF1505
ORF1506
ORF1507
ORF1508
ORF1509
ORF1510
ORF1511
ORF1512
ORF1513
ORF1514
ORF1515
ORF1516
ORF1517
ORF1518
ORF1519
ORF1520
ORF1521
ORF1522
ORF1523
ORF1524
ORF1525
ORF1526
ORF1527
ORF1528
ORF1529
ORF1530
ORF1531
ORF1532
ORF1533
ORF1534
ORF1535
ORF1536
ORF1537
ORF1538
ORF1539
ORF1540
ORF1541
ORF1542
ORF1543
ORF1544
ORF1545
ORF1546
ORF1547
ORF1548
ORF1549
ORF1550
ORF1551
ORF1552
ORF1553
ORF1554
ORF1555
ORF1556
ORF1557
ORF1558
ORF1559
ORF1560
ORF1561
ORF1562
ORF1563
ORF1564
ORF1565
ORF1566
ORF1567
ORF1568
ORF1569
ORF1570
ORF1571
ORF1572
ORF1573
ORF1574
ORF1575
ORF1576
ORF1577
ORF1578
ORF1579
ORF1580
ORF1581
ORF1582
ORF1583
ORF1584
ORF1585
ORF1586
ORF1587
ORF1588
ORF1589
ORF1590
ORF1591
ORF1592
ORF1593
ORF1594
ORF1595
ORF1596
ORF1597
ORF1598
ORF1599
ORF1600
ORF1601
ORF1602
ORF1603
ORF1604
ORF1605
ORF1606
ORF1607
ORF1608
ORF1609
ORF1610
ORF1611
ORF1612
ORF1613
ORF1614
ORF1615
ORF1616
ORF1617
ORF1618
ORF1619
ORF1620
ORF1621
ORF1622
ORF1623
ORF1624
ORF1625
ORF1626
ORF1627
ORF1628
ORF1629
ORF1630
ORF1631
ORF1632
ORF1633
ORF1634
ORF1635
ORF1636
ORF1637
ORF1638
ORF1639
ORF1640
ORF1641
ORF1642
ORF1643
ORF1644
ORF1645
ORF1646
ORF1647
ORF1648
ORF1649
ORF1650
ORF1651
ORF1652
ORF1653
ORF1654
ORF1655
ORF1656
ORF1657
ORF1658
ORF1659
ORF1660
ORF1661
ORF1662
ORF1663
ORF1664
ORF1665
ORF1666
ORF1667
ORF1668
ORF1669
ORF1670
ORF1671
ORF1672
ORF1673
ORF1674
ORF1675
ORF1676
ORF1677
ORF1678
ORF1679
ORF1680
ORF1681
ORF1682
ORF1683
ORF1684
ORF1685
ORF1686
ORF1687
ORF1688
ORF1689
ORF1690
ORF1691
ORF1692
ORF1693
ORF1694
ORF1695
ORF1696
ORF1697
ORF1698
ORF1699
ORF1700
ORF1701
ORF1702
ORF1703
ORF1704
ORF1705
ORF1706
ORF1707
ORF1708
ORF1709
ORF1710
ORF1711
ORF1712
ORF1713
ORF1714
ORF1715
ORF1716
ORF1717
ORF1718
ORF1719
ORF1720
ORF1721
ORF1722
ORF1723
ORF1724
ORF1725
ORF1726
ORF1727
ORF1728
ORF1729
ORF1730
ORF1731
ORF1732
ORF1733
ORF1734
ORF1735
ORF1736
ORF1737
ORF1738
ORF1739
ORF1740
ORF1741
ORF1742
ORF1743
ORF1744
ORF1745
ORF1746
ORF1747
ORF1748
ORF1749
ORF1750
ORF1751
ORF1752
ORF1753
ORF1754
ORF1755
ORF1756
ORF1757
ORF1758
ORF1759
ORF1760
ORF1761
ORF1762
ORF1763
ORF1764
ORF1765
ORF1766
ORF1767
ORF1768
ORF1769
ORF1770
ORF1771
ORF1772
ORF1773
ORF1774
ORF1775
ORF1776
ORF1777
ORF1778
ORF1779
ORF1780
ORF1781
ORF1782
ORF1783
ORF1784
ORF1785
ORF1786
ORF1787
ORF1788
ORF1789
ORF1790
ORF1791
ORF1792
ORF1793
ORF1794
ORF1795
ORF1796
ORF1797
ORF1798
ORF1799
ORF1800
ORF1801
ORF1802
ORF1803
ORF1804
ORF1805
ORF1806
ORF1807
ORF1808
ORF1809
ORF1810
ORF1811
ORF1812
ORF1813
ORF1814
ORF1815
ORF1816
ORF1817
ORF1818
ORF1819
ORF1820
ORF1821
ORF1822
ORF1823
ORF1824
ORF1825
ORF1826
ORF1827
ORF1828
ORF1829
ORF1830
ORF1831
ORF1832
ORF1833
ORF1834
ORF1835
ORF1836
```



```

/organism="Populus tremula x Populus tremuloides"
/mol_type="genomic DNA"
/cultivar="Eschs"
/isolate="SK414"
/db_xref="taxon:47664"
/sex="female"
/tissue_type="leaf"
/transgenic
/notes="transgenic line Eschs:358-AC-rolc#3"
source 1..107
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
repeat_region <1..107
/transposon="Ac element"
N
ary Match 14.9%; Score 40.4; DB 12; Length 197;
t Local Similarity 71.6%; Pred. No. 0.029;
ches 53; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
65 AGGGATGAAACGGTCGGTACGGTCGGTAAATACATACGGGATTTTCCATCCTACTT 124
|||||
106 AGGGATGAAACGGTCGGTACGGTCGGTAAATACATCTCTACCGTTTTCATTCATATT 47
|||||
125 TCATCCGGGCTAC 138
|||||
46 TTAACCTCGGGAC 33
|||||
.T 14
; 779/c
AY201779 407 bp DNA linear SYN 27-MAY-2003
Arabidopsis thaliana sequence flanking Ds3 end of Ds-Trap insertion
from line GT5331.
SSION AY201779
CON AY201779.1 GI:27897733
XRDs
EE
ANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.
RENCE 1 (bases 1 to 407)
MAY.B.P., Simorowski,J., Arroyo,J.-M., Vaughn,M.W., Shen,R.,
McCombie,W.R. and Martienssen,R.A.
Arabidopsis genomic sequences flanking Ds enhancer and gene traps
in transgenic lines
Unpublished
RENCE 2 (bases 1 to 407)
MAY.B.P., Simorowski,J., Arroyo,J.-M., Vaughn,M.W., Shen,R.,
McCombie,W.R. and Martienssen,R.A.
Direct Submission
FILE Submitted (17-DEC-2002) Cold Spring Harbor Laboratory, 1 Bungtown
Road, Cold Spring Harbor, NY 11724, USA
http://genetrap.cchl.org
Location/Qualifiers
1..407
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GT5331.Ds3.04.00.b.407"
/ecotype="Landsberg"
/transgenic
/notes="transgenic line GT5331"
source 1..36
/organism="Zea mays"
/mol_type="genomic DNA"
/db_xref="taxon:4577"
repeat_region <1..36
/transposon="transposon Ds"

```

This Page Blank (uspio)

iclcic - nucleic search, using sw model

m: May 16, 2004, 10:18:15 ; Search time 397 Seconds
(without alignments)

2899.903 Million cell updates/sec

US-09-701-023-2

ct score: 271

nce: 1 gtagcatgcatcttaacaa.....ctactcatgagctctcttca 271

ng table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

hed: 3373863 seqs, 2124099041 residues

. number of hits satisfying chosen parameters: 6747726

num DB seq length: 0

num DB seq length: 2000000000

-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

ase : N_Geneseq_29Jan04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001as.*

5: Geneseq2001bs.*

6: Geneseq2002s.*

7: Geneseq2003as.*

8: Geneseq2003bs.*

9: Geneseq2003cs.*

10: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lt	o.	Score	Query Match	Length	DB ID	Description
1	1	271	100.0	271	3	AAA94066 Arabidops
2	2	127.4	47.0	1302	3	AAA94065 Arabidops
3	3	127.4	47.0	4071	3	AAA94067 Arabidops
4	4	39.4	14.5	4810	7	ABX93341 DNA encod
5	5	39	14.4	4565	7	AAI65447 Nucleotid
6	6	39	14.4	4565	7	ABX93342 Transposa
7	7	32.4	12.0	495	5	AA578905 DNA encod
8	8	31.6	11.7	2692	4	ABL19247 Drosophil
9	9	31.6	11.7	2971	4	ABL28815 Drosophil
10	10	31.6	11.7	3037	4	ABL20065 Drosophil
11	11	31.6	11.7	3308	4	ABL28824 Drosophil
12	12	31.6	11.7	10400	4	ABL20064 Drosophil
13	13	31.6	11.7	10418	4	ABL28814 Drosophil
14	14	31.6	11.7	10451	4	ABL19246 Drosophil
15	15	30.8	11.4	1395	6	ABQ79896 Chicken a
16	16	30.8	11.4	2065	6	ABQ79903 Chicken a
17	17	30.8	11.4	5769	4	AAK83560 Human inm
18	18	30.8	11.4	6162	4	AAK83551 Human inm
19	19	30.8	11.4	6168	4	AAK83557 Human inm
20	20	30.8	11.4	6232	4	AAK83552 Human inm
21	21	30.8	11.4	6259	4	AAK83559 Human inm
22	22	30.8	11.4	6261	4	AAK83554 Human inm
23	23	30.2	11.1	1022	4	AAH34871 Human col

ALIGNMENTS

RESULT 1

AAA94066

ID AAA94066 standard; DNA; 271 BP.

XX AAA94066;

AC AAA94066;

XX 30-JAN-2001 (first entry)

DT Arabidopsis thaliana sporocytless spl Ds element sequence.

DE Sporocytless; spl; meiocyte formation; plant sterility; seedless fruit;

DE pollenless flower; Ds element; ds.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX Key Location/Qualifiers

PH misc_feature /tag= a

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 64. .133

FT /tag= c

FT /note= "Ds element"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

FT /tag= b

FT /note= "4 base pair duplication due to Ds element

FT insertion"

FT 134. .137

instant invar
parent

Ye D, Yang W, Sundaresan V, Xu J;
WPI; 2000-594578/56.

Sporocytless nucleic acids and polypeptides, useful for controlling sporocyte or metocyte formation in plants for producing transgenics that bear seedless fruits and/or pollenless flowers.

Claim 45; Fig 5; 65pp; English.

The present sequence comprises the promoter and coding sequence for the Arabidopsis thaliana sporocytless (SPL) protein. This protein is involved in the formation of microsporocytes in male plants and megasporocytes in female plants. The mutant gene was isolated from a collection of transposants due to its male and female sterile phenotype. The mutation is caused by the insertion of the Ds element between bases 411 and 412 of the gene, causing a 4 base pair duplication. The identification of the sterile phenotype in plants caused by the insertion of this element means that it can be used to produce transgenic plants which contain the Ds element or antisense sequences to the gene, enabling the production of seedless fruits, pollenless flowers and plants with a larger biomass

Sequence 4071 BP; 1306 A; 742 C; 692 G; 1331 T; 0 U; 0 Other;

Query Match 47.0%; Score 127.4; DB 3; Length 4071;
Best Local Similarity 98.6%; Pred. No. 2.7e-35;
Matches 139; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
132 GGGCTACAGGCTTCCCAAGTCA-TCGGAGCAACAGAGTCTATTGTGGAGTCGGG 190
3020 GTGCTACAGGCTTCCCAAGTCACTCGGAGCAACAGAGTCTATTGTGGAGTCGGG 3079
191 TCGGCTCAGGTTATGATGACCCGCTTATTTCTCATCGGCTTGTGAGACCTCC 250
3080 TCGGCTCAGGTTATGATGACCCGCTTATTTCTCATCGGCTTGTGAGACCTCC 3139
251 ACTACTCATGAGTCTCTTCA 271
3140 ACTACTCATGAGTCTCTTCA 3160

LT 4
3541
ABX93541 standard; DNA; 4810 BP.
ABX93541;

06-JUN-2003 (first entry)

DNA encoding the maize transposable element activator (Ac9).

Maize; ds; transposable element activator; transcription modification; gene repression; antibiotic resistance; human gamete; transplacental; shoot; heart disease; phenylketonuria; Alzheimer's disease; aging; emphysema; cancer; osteoporosis; diabetes; sleep apnea; sickle cell anaemia; stroke; multiple sclerosis; muscular dystrophy; bursitis; diverticular disease; glaucoma; blindness; cataract; attention deficit disorder; dyslexia; hypertension; schizophrenia; depression; bulimia nervosa; migraine; anorexia nervosa; heart attack; allergy; baldness; metabolic disorder; blood clotting; haemophilia; thalassaemia; neuromuscular disease; AC9; pregnancy associated disease; erectile dysfunction; infertility; obesity; immune system disorder; blood cell surface antigen recognition disease; nondisjunction; epilepsy; gastroenteritis; spinal cord disorder; pituitary gland disorder; Parkinson's disease; osteoarthritis; cystic fibrosis; arterial disease; mania; cardiomyopathy; waxy locus.

Zea mays.

US2002199216-A1.

26-DEC-2002.

XX 01-MAY-2002; 2002US-00138221.
XX PF
XX 01-MAY-2001; 2001US-0287882P.
XX PA
XX (MACR/) MACRAE A P.
XX PI
XX Macrae AF;
XX WPI; 2003-329235/31.

Modifying transcription within an organism or repressing transcription of targeted gene within a cell, by introducing transposase-encoding effector molecule into organism or introducing transposase element into cell.

Disclosure; Page 30-33; 46pp; English.

The invention relates to a method of modifying (increasing, decreasing or altering) transcription within an organism or repressing transcription of at least one targeted gene within a cell comprising introducing a transposase-encoding effector molecule into the organism or introducing a transposase element into the cell. The method is useful for modifying a (increasing, decreasing or altering) transcription within an organism or for repressing transcription of at least one targeted gene within a cell. The method is useful for determining the functions of unknown function genes within an organism. The method is useful for repressing transcription within an organism e.g. transcription of a gene encoding antibiotic resistance, for repressing targeted genes within human gametes (sperm and egg). The method is useful for repressing transcription within an in vitro cell system. The method is useful for repressing transcription during the cell cycle. The method is also useful for repressing transcription within a transplanted organ, shoot, or body part. The method is also useful for modifying the expression of genes associated with heart disease, phenylketonuria, Alzheimer's disease, aging, cancer, osteoporosis, diabetes, sleep apnea, sickle cell anaemia, multiple sclerosis, muscular dystrophy, bursitis, emphysema, diverticular disease, glaucoma, blindness, cataracts, attention deficit disorder, dyslexia, hypertension, schizophrenia, mania, depression, bulimia nervosa, anorexia nervosa, stroke, heart attack, allergies, migraine, baldness, metabolic disorders, blood clotting, haemophilia, thalassaemia, neuromuscular diseases, diseases of pregnancy, erectile dysfunction, infertility, immune system disorders, blood cell surface antigen recognition disease, nondisjunction, epilepsy, obesity, gastroenteritis, spinal cord disorders, pituitary gland disorders, Parkinson's disease, osteoarthritis, cystic fibrosis, arterial disease and cardiomyopathy. The present sequence represents DNA encoding the maize transposable element activator (Ac9) from the waxy locus

SQ Sequence 4810 BP; 1390 A; 1063 C; 1063 G; 1294 T; 0 U; 0 Other;

Query Match 14.5%; Score 39.4; DB 7; Length 4810;
Best Local Similarity 75.4%; Pred. No. 0.0033;
Matches 49; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 63 ACAGGATGAAACCGTCGGTAACCGTCGGTAATAATACTACGGGATTTTCCCATCTAC 122
Db 121 ATAGGATGAAACCGTCGGTAACCGTCGGTAATAATACTACCGGTTTTCATTTTCATA 180
QY 123 TTTC 127
Db 181 TTAA 185

RESULT 5
AAI65447
ID AAI65447 standard; DNA; 4565 BP.
XX AAI65447;
XX 10-DEC-2001 (first entry)

XX Nucleotide sequence of a maize activator element (Ac).

Too Late

KW Activator element; Ac; transposable element; Ds element; transposon;
 KW gamete-specific promoter; suicide gene; gametophytic suicide trait; GST;
 KW ss.
 XX
 XX Zea mays.
 XX
 XX W0200164926-A2.
 XX
 XX 07-SEP-2001.
 XX
 XX 28-FEB-2001; 2001WO-US006249.
 XX
 XX 28-FEB-2000; 2000US-0185524P.
 XX
 XX (UYUA) UNIV YALE.
 XX
 XX Dellaporta SL, Moreno MA;
 XX
 XX WPI; 2001-602568/68.
 XX
 XX Genetic construct for the control of transgenes in transgenic plants
 XX comprises a sex-specific promoter operatively linked to a suicide gene
 XX that selects against male or female gametes containing the suicide gene.
 XX
 XX Example 1; Page 73-74; 81pp; English.
 XX
 XX The present sequence represents a maize Activator element (Ac), which is
 XX a transposable element. 5' and 3' fragments of the present sequence were
 XX combined by cloning to produce a synthetic Ds element, which was used to
 XX produce the construct of the invention. The specification describes a
 XX nucleic acid construct, comprising a male gamete- or female gamete-
 XX specific promoter operably linked to a suicide gene, both of which are
 XX linked to a gene of interest, a transposable element, a transposon and
 XX the encoding nucleic acid. The construct controls the unwanted spread of
 XX heterologous traits in plants. It also provides genetic systems which can
 XX be used for the elimination of a gametophytic suicide trait (GST) and for
 XX the selection of unlinked transpositions. The construct is applicable for
 XX any commercially grown plant, including fruit, seed, oil, protein or hay
 XX production, animal grazing, golf courses, lawns, erosion control,
 XX landscaping, green manure, producing food additives, pulp and wood
 XX production and smoking products
 XX
 XX Sequence 4565 BP; 1344 A; 994 C; 978 G; 1249 T; 0 U; 0 Other;

Query Match 14.4%; Score 39; DB 4; Length 4565;
 Best Local Similarity 76.2%; Pred. No. 0.0045;
 Matches 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 65 AGGATGAAAACGGTCGGTAACGGTCGGTAACCGTAAATACCTACCGGATTTTCCATCTACTT 124
 DB 2 AGGATGAAAACGGTCGGTAACGGTCGGTAACCGTAAATACCTACCGGATTTTCCATCTACTT 61
 QY 125 TCA 127
 DB 62 TAA 64

RESULT 6
 ID ABX93542/c
 XX ABX93542 standard; DNA; 4565 BP.
 XX
 XX AC ABX93542;
 XX
 XX 06-JUN-2003 (first entry)
 XX
 XX Transposable element associated nucleic acid.

ds; transcription modification; gene repression; antibiotic resistance;
 human gamete; transposon; shoot; heart disease; phenylketonuria;
 Alzheimer's disease; aging; emphysema; cancer; osteoporosis; diabetes;
 sleep apnea; sickle cell anemia; stroke; multiple sclerosis;
 muscular dystrophy; bursitis; diverticular disease; glaucoma; blindness;
 cataract; attention deficit disorder; dyslexia; hypertension;

KW schizophrenia; depression; bulimia nervosa; migraine; anorexia nervosa;
 KW heart attack; allergy; baldness; metabolic disorder; blood clotting;
 KW haemophilia; thalassemia; neuromuscular disease; erectile dysfunction;
 KW pregnancy associated disease; infertility; obesity; gastroenteritis;
 KW immune system disorder; blood cell surface antigen recognition disease;
 KW nondisjunction; epilepsy; spinal cord disorder; pituitary gland disorder;
 KW Parkinson's disease; osteoarthritis; cystic fibrosis; arterial disease;
 KW mania; cardiomyopathy.
 XX
 XX Unidentified.

US2002199216-A1.

26-DEC-2002.

01-MAY-2002; 2002US-00138221.

01-MAY-2001; 2001US-0287882P.

(MACR/) MACRAE A F.

Macrae AF;

WPI; 2003-329235/31.

Modifying transcription within an organism or repressing transcription of
 targeted gene within a cell, by introducing transposase-encoding effector
 molecule into organism or introducing transposase element into cell.

Disclosure; Page 34-37; 46pp; English.

XX The invention relates to a method of modifying (increasing, decreasing or
 altering) transcription within an organism or repressing transcription of
 at least one targeted gene within a cell comprising introducing a
 transposase-encoding effector molecule into the organism or introducing a
 transposase element into the cell. The method is useful for modifying
 (increasing, decreasing or altering) transcription within an organism or
 for repressing transcription of at least one targeted gene within a cell.
 The method is useful for determining the functions of unknown function
 genes within an organism. The method is useful for repressing
 transcription within an organism e.g. transcription of a gene encoding
 antibiotic resistance, for repressing targeted genes within human gametes
 (sperm and egg). The method is useful for repressing transcription within
 an in vitro cell system. The method is useful for repressing
 transcription during the cell cycle. The method is also useful for
 repressing transcription within a transplanted organ, shoot, or body
 part. The method is also useful for modifying the expression of genes
 associated with heart disease, phenylketonuria, Alzheimer's disease,
 aging, cancer, osteoporosis, diabetes, sleep apnea, sickle cell anemia,
 multiple sclerosis, muscular dystrophy, bursitis, emphysema, diverticular
 disease, glaucoma, blindness, cataracts, attention deficit disorder,
 dyslexia, hypertension, schizophrenia, mania, depression, bulimia
 nervosa, anorexia nervosa, stroke, heart attack, allergies, migraine,
 baldness, metabolic disorders, blood clotting, haemophilia,
 chalassemia, neuromuscular diseases, diseases of pregnancy, erectile
 dysfunction, infertility, immune system disorders, blood cell surface
 antigen recognition disease, nondisjunction, epilepsy, obesity,
 gastroenteritis, spinal cord disorders, pituitary gland disorders,
 Parkinson's disease, osteoarthritis, cystic fibrosis, arterial disease
 and cardiomyopathy. The present sequence represents the transposable
 element associated nucleic acid. Note: the present sequence is shown in
 the appendix of the specification but no reference is made to it
 elsewhere in the specification

Sequence 4565 BP; 1249 A; 978 C; 994 G; 1344 T; 0 U; 0 Other;

Query Match 14.4%; Score 39; DB 7; Length 4565;
 Best Local Similarity 76.2%; Pred. No. 0.0045;
 Matches 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 65 AGGATGAAAACGGTCGGTAACGGTCGGTAACCGTAAATACCTACCGGATTTTCCATCTACTT 124
 DB 4564 AGGATGAAAACGGTCGGTAACGGTCGGTAACCGTAAATACCTACCGGATTTTCCATCTACTT 4505

too late

: 40 CCGGTAGACCCCGGTGTTGTGCTACAGGATGAAACCGTCCGTAAACGGTCGGTAAATA 99

2559

COLLIER

2559

```
OY      247 CTCACACTACTCATG 260
DB      2560 GTCCCATCTCATG 2573
|||||
|||||

RESULT 9
ABL28815
ID      ABL28815 standard; DNA; 2971 BP.
XX
AC      ABL28815;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Drosophila melanogaster genomic polynucleotide SEQ ID NO 37918.
XX
KW      Drosophila; developmental biology; cell signalling; insecticide;
KW      pharmaceutical; gene; ds.
XX
OS      Drosophila melanogaster.
XX
PN      WO200171042-A2.
XX
PD      27-SEP-2001.
XX
PF      23-MAR-2001; 2001WO-US009231.
XX
PR      23-MAR-2000; 2000US-0191637P.
XX
PR      11-JUL-2000; 2000US-00614150.
XX
PA      (PEKE ) PE CORP NY.
XX
PI      Venter JC, Adams M, Li PWD, Myers EW;
XX
WPI; 2001-656860/75.
XX
New isolated nucleic acid detection reagent for detecting 1000 or more
PT      genes from Drosophila and for elucidating cell signalling and cell-cell
PT      interactions.
XX
PS      Claim 1; SEQ ID NO 37918; 21pp + Sequence Listing; English.
XX
The invention relates to an isolated nucleic acid detection reagent
CC      capable of detecting 1000 or more genes from Drosophila. The invention is
CC      useful in developmental biology and in elucidating cell signalling and
CC      cell-cell interactions in higher eukaryotes for the development of
CC      insecticides, therapeutics and pharmaceutical drugs. The invention
CC      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC      sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
CC      ABB72072). The sequence data for this patent did not form part of the
CC      printed specification, but was obtained in electronic format directly
CC      from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 2971 BP; 719 A; 888 C; 744 G; 620 T; 0 U; 0 Other;

Query Match      11.7%; Score 31.6; DB 4; Length 2971;
Best Local Similarity 52.2%; Pred. No. 1.9;
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

OY      127 ATCCGGGCTACAAGCTTCCCAAGTCATCGGAGCAACAGGATCTATTGTGGTGAGT 186
DB      2719 ATCAAGCATCATGTGCGCAGCCACAGCCGCGGAGCAACAGGACCCAGCTGATC 2778
|||||
|||||
|||||

OY      187 CGGGTCGGGTGAGTTATGATGACCCGGGTATTTCTCCATGGGGTTTGTGAGACCTC 246
DB      2779 CGCCCGGAGCTGGTATCATGACCCAGGCGGATTCGATGCTCTCTGAGCGTGCTC 2838
|||||
|||||
|||||

OY      247 CTCACACTACTCATG 260
DB      2839 GTCCCATCTCATG 2852
|||||
|||||

RESULT 10
ABL20065
ID      ABL20065 standard; DNA; 3037 BP.
XX
AC      ABL20065;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Drosophila melanogaster genomic polynucleotide SEQ ID NO 11668.
XX
KW      Drosophila; developmental biology; cell signalling; insecticide;
KW      pharmaceutical; gene; ds.
XX
OS      Drosophila melanogaster.
XX
PN      WO200171042-A2.
XX
PD      27-SEP-2001.
XX
PF      23-MAR-2001; 2001WO-US009231.
XX
PR      23-MAR-2000; 2000US-0191637P.
XX
PR      11-JUL-2000; 2000US-00614150.
XX
PA      (PEKE ) PE CORP NY.
XX
PI      Venter JC, Adams M, Li PWD, Myers EW;
XX
WPI; 2001-656860/75.
XX
New isolated nucleic acid detection reagent for detecting 1000 or more
PT      genes from Drosophila and for elucidating cell signalling and cell-cell
PT      interactions.
XX
PS      Claim 1; SEQ ID NO 11668; 21pp + Sequence Listing; English.
XX
The invention relates to an isolated nucleic acid detection reagent
CC      capable of detecting 1000 or more genes from Drosophila. The invention is
CC      useful in developmental biology and in elucidating cell signalling and
CC      cell-cell interactions in higher eukaryotes for the development of
CC      insecticides, therapeutics and pharmaceutical drugs. The invention
CC      discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC      sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
CC      ABB72072). The sequence data for this patent did not form part of the
CC      printed specification, but was obtained in electronic format directly
CC      from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ      Sequence 3037 BP; 743 A; 876 C; 753 G; 665 T; 0 U; 0 Other;

Query Match      11.7%; Score 31.6; DB 4; Length 3037;
Best Local Similarity 52.2%; Pred. No. 1.9;
Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

OY      127 ATCCGGGCTACAAGCTTCCCAAGTCATCGGAGCAACAGGATCTATTGTGGTGAGT 186
DB      2785 ATCAAGCATCATGTGCGCAGCCACAGCCGCGGAGCAACAGGACCCAGCTGATC 2844
|||||
|||||
|||||

OY      187 CGGGTCGGGTGAGTTATGATGACCCGGGTATTTCTCCATGGGGTTTGTGAGACCTC 246
DB      2845 CGCCCGGAGCTGGTATCATGACCCAGGCGGATTCGATGCTCTCTGAGCGTGCTC 2904
|||||
|||||
|||||

OY      247 CTCACACTACTCATG 260
DB      2905 GTCCCATCTCATG 2918
|||||
|||||

RESULT 11
ABL28824/c
ID      ABL28824 standard; DNA; 3308 BP.
XX
AC      ABL28824;
XX
DT      26-MAR-2002 (first entry)
XX
DE      Drosophila melanogaster genomic polynucleotide SEQ ID NO 37945.
```

XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX PI WPI; 2001-656860/75.
 XX DR New isolated nucleic acid detection reagent for detecting 1000 or more
 XX PT genes from Drosophila and for elucidating cell signaling and cell-cell
 XX PT interactions.
 XX XX Claim 1; SEQ ID NO 11665; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
 XX CC useful in developmental biology and in elucidating cell signalling and
 XX CC cell-cell interactions in higher eukaryotes for the development of
 XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
 XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 XX CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 XX CC ABBS72072). The sequence data for this patent did not form part of the
 XX CC printed specification, but was obtained in electronic format directly
 XX CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 10400 BP; 2886 A; 2139 C; 2340 G; 3035 T; 0 U; 0 Other;

Query Match 11.7%; Score 31.6; DB 4; Length 10400;
 Best Local Similarity 52.2%; Pred. No. 3.2; Indels 0; Gaps 0;
 Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 127 ATCCCGGCTACAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGAGT 186
 DB 1253 ATCAACGACATCATCGTCCAGCCGACAGCCGACAGCAGCAGCCAGCTGATC 1194
 QY 187 CGGTCGGGTGAGGTTATGATCGACCCGGTTATTCTCCATGGGGTTTGTGAGACCTC 246
 DB 1193 CGCGCCGAGCTGGCTATCAGCCAGCGGCGATTCGATGTCCTTCTTGAGCGGTGCTC 1134
 QY 247 CTCCTACTACTCATG 260
 DB 1133 GTCCCCATCTCATG 1120
 RESULT 13
 ABL28814/c
 ID ABL28814 standard; DNA; 10418 BP.
 XX AC ABL28814;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 37915.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical; gene; ds.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.

Drosophila; developmental biology; cell signalling; insecticide;
 pharmaceutical; gene; ds.
 Drosophila melanogaster.
 WO200171042-A2.
 27-SEP-2001.
 23-MAR-2001; 2001WO-US009231.
 23-MAR-2000; 2000US-0191637P.
 11-JUL-2000; 2000US-00614150.
 (PEKE) PE CORP NY.
 Venter JC, Adams M, Li PWD, Myers EW;
 WPI; 2001-656860/75.
 New isolated nucleic acid detection reagent for detecting 1000 or more
 genes from Drosophila and for elucidating cell signaling and cell-cell
 interactions.
 Claim 1; SEQ ID NO 37945; 21pp + Sequence Listing; English.
 The invention relates to an isolated nucleic acid detection reagent
 capable of detecting 1000 or more genes from Drosophila. The invention is
 useful in developmental biology and in elucidating cell signalling and
 cell-cell interactions in higher eukaryotes for the development of
 insecticides, therapeutics and pharmaceutical drugs. The invention
 discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 ABBS72072). The sequence data for this patent did not form part of the
 printed specification, but was obtained in electronic format directly
 from WIPO at ftp.wipo.int/pub/published_pct_sequences
 Sequence 3308 BP; 898 A; 727 C; 732 G; 951 T; 0 U; 0 Other;
 Query Match 11.7%; Score 31.6; DB 4; Length 3308;
 Best Local Similarity 52.2%; Pred. No. 2;
 Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 127 ATCCCGGCTACAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGAGT 186
 DB 2887 ATCAACGACATCATCGTCCAGCCGACAGCCGACAGCAGCAGCCAGCTGATC 2828
 QY 187 CGGTCGGGTGAGGTTATGATCGACCCGGTTATTCTCCATGGGGTTTGTGAGACCTC 246
 DB 2827 CGCGCCGAGCTGGCTATCAGCCAGCGGCGATTCGATGTCCTTCTTGAGCGGTGCTC 2768
 QY 247 CTCCTACTACTCATG 260
 DB 2767 GTCCCCATCTCATG 2754
 RESULT 12
 ABL20064/c
 ID ABL20064 standard; DNA; 10400 BP.
 XX AC ABL20064;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 11665.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical; gene; ds.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.

XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 XX
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 XX Claim 1; SEQ ID NO 37915; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 10418 BP; 2894 A; 2143 C; 2343 G; 3038 T; 0 U; 0 Other;
 SQ
 Query Match 11.7%; Score 31.6; DB 4; Length 10418;
 Best Local Similarity 52.2%; Pred. No. 3.3;
 Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 127 ATCCCGGCTACAGGCTTCCCAAGCTCATCGGAGCAACAGATCTATTGTGGAGT 186
 DB 1253 ATCAACGACATCATCGTGGCCACGCGCCAGCAGCAGCAGCAGCAGCAGTGC 1194
 QY 187 CGGGTCGGGTGAGTATGATCGACCGGTTATTTCTCCATGGGTTTGTGACACTC 246
 DB 1193 CGCCCGGAGTGGTATGAGCAGCGCGGATTTTCGATGTTCTTCTGAGCGGTGCTC 1134
 QY 247 CTCCTACTCTCATG 260
 DB 1133 GTCCCATCTCATG 1120
 RESULT 14
 ABL19246/c
 ID ABL19246 standard; DNA; 10451 BP.
 XX
 XX ABL19246;
 AC
 XX 26-MAR-2002 (first entry)
 DT
 XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 9211.
 DE
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical; gene; ds.
 XX
 XX Drosophila melanogaster.
 OS
 XX WO200171042-A2.
 PN
 XX 27-SEP-2001.
 PD
 XX 23-MAR-2001; 2001WO-US009231.
 PP
 XX 23-MAR-2000; 2000US-0191637P.
 PR
 XX 11-JUL-2000; 2000US-00614150.
 XX
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 PI WPI; 2001-656860/75.
 XX
 XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX
 XX Claim 1; SEQ ID NO 9211; 21pp + Sequence Listing; English.
 PS
 XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 10451 BP; 2904 A; 2145 C; 2346 G; 3056 T; 0 U; 0 Other;
 SQ
 Query Match 11.7%; Score 31.6; DB 4; Length 10451;
 Best Local Similarity 52.2%; Pred. No. 3.3;
 Matches 70; Conservative 0; Mismatches 64; Indels 0; Gaps 0;
 QY 127 ATCCCGGCTACAGGCTTCCCAAGCTCATCGGAGCAACAGATCTATTGTGGAGT 186
 DB 1253 ATCAACGACATCATCGTGGCCACGCGCCAGCAGCAGCAGCAGCAGTGC 1194
 QY 187 CGGGTCGGGTGAGTATGATCGACCGGTTATTTCTCCATGGGTTTGTGACACTC 246
 DB 1193 CGCCCGGAGTGGTATGAGCAGCGCGGATTTTCGATGTTCTTCTGAGCGGTGCTC 1134
 QY 247 CTCCTACTCTCATG 260
 DB 1133 GTCCCATCTCATG 1120
 RESULT 15
 ABQ79896/c
 ID ABQ79896 standard; cDNA; 1395 BP.
 XX
 XX ABQ79896;
 AC
 XX 23-DEC-2002 (first entry)
 DT
 XX Chicken acetylglucosamine transferase VI (Gnt VI) protein encoding cDNA.
 DE
 XX Acetylglucosamine transferase VI; Gnt VI; GlcNAc; N-glucan; chicken;
 KW gene; ss.
 XX
 XX Gallus gallus.
 OS
 XX Key Location/Qualifiers
 FT CDS 1..1395
 FT /*tag= a
 FT /product= "Gnt VI"
 FT /note= "acetylglucosamine transferase VI protein"
 XX
 XX JP2002209587-A.
 PN
 XX 30-JUL-2002.
 PD
 XX 18-JAN-2001; 2001JP-00010883.
 PP
 XX 18-JAN-2001; 2001JP-00010883.
 PR
 XX (EURE) FUJIREBIO KK.
 PA
 XX WPI; 2002-670039/72.
 DR P-FSDB; ABB82145.
 XX
 XX An acetylglucosamine transferase VI protein.
 PT
 XX Claim 5; Page 11-13; 22pp; Japanese.
 PS

The invention relates to a protein having acetylglucosamine transferase VI (Gnt VI) activity and polynucleotides encoding the Gnt VI protein. The protein can be expressed by standard recombinant methodology. Gnt VI is useful for catalysing the transfer of GlcNAc to the 4th site of Man alpha 1,6 arm of the core structure of N-glycan. The present sequence represents the chicken Gnt VI protein coding sequence

Sequence 1395 BP; 280 A; 444 C; 366 G; 305 T; 0 U; 0 Other;
ry Match 11.4%; Score 30.8; DB 6; Length 1395;
t Local Similarity 48.8%; Pred. No. 2.6;
ches 83; Conservative 0; Mismatches 87; Indels 0; Gaps 0;
35 CCGTACCGGTAGACCCGGGTTGTGCTACAGGATGAAACGGTCGGTAACGGTCGGTA 94
1143 CTGCACCGGACCGGGTGACACGGGCTGGTTGGTGAAGACAATGGAGAAATGCTGCC 1084
95 AAATACTACGGGATTTTCCCATCTACTTTCATCCGGGCTACAGGCTTCCCAAGCTC 154
1083 AACTGCTGGGTTTTTCCCCAGAAATACCCCTTGCCTGTGTGTAAGCCTTGGAGGGCTC 1024
155 ATCGGGAGCAACAGATCTATTGTGGTGGAGTCGGGTCGGGTCAGGTTAT 204
1023 ATAGTTCTCAAGACACCACTGTTGGTGAACAGGGCTCTGGCGGTTGT 974

h completed: May 16, 2004, 13:08:25
ime : 403 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

iclcic - nucleic search, using sw model

m: May 16, 2004, 12:43:45 ; Search time 75 Seconds
(without alignments)
2005.223 Million cell updates/sec

ct score: 271

mce: 1 gtagcatgcgtctctaa...ctactcatgagctctcttca 271

ng table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

hed: 682709 seqs, 277475446.residues

number of hits satisfying chosen parameters: 1365418

um DB seq length: 0

um DB seq length: 2000000000

processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

base :

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/pttus_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

t	Score	Query Match	Length	DB	ID	Description
1	29	10.7	5992	2	US-08-475-891A-3	Sequence 3, Appli
2	27.4	10.1	777	4	US-09-252-991A-12771	Sequence 12771, A
3	27.4	10.1	1008	4	US-09-252-991A-13017	Sequence 13017, A
4	27.4	10.1	2577	4	US-09-252-991A-13185	Sequence 13185, A
5	27.4	10.1	53332	4	US-09-801-861-3	Sequence 3, Appli
6	27.4	10.1	151652	4	US-09-497-855A-40	Sequence 40, Appli
7	27.2	10.0	948	4	US-09-252-991A-12220	Sequence 12220, A
8	27	10.0	474	4	US-09-621-976-18033	Sequence 18033, A
9	27	10.0	1074	4	US-09-134-001C-2128	Sequence 2128, App
10	27	10.0	3001	4	US-09-539-333D-127	Sequence 127, App
11	27	10.0	111282	4	US-09-754-250-3	Sequence 3, Appli
12	26.8	9.9	832	4	US-09-621-976-2813	Sequence 2813, Ap
13	26.8	9.9	903	3	US-08-829-525-37	Sequence 37, Appl
14	26.8	9.9	903	3	US-08-609-583A-37	Sequence 37, Appl
15	26.8	9.9	903	3	US-08-937-399-37	Sequence 37, Appl
16	26.8	9.9	903	4	US-09-310-367-37	Sequence 37, Appl
17	26.8	9.9	903	4	US-09-032-337-37	Sequence 37, Appl
18	26.8	9.9	903	4	US-09-464-231-37	Sequence 37, Appl
19	26.8	9.9	2236	3	US-08-829-525-23	Sequence 23, Appl
20	26.8	9.9	2236	3	US-08-609-583A-23	Sequence 23, Appl
21	26.8	9.9	2236	3	US-08-937-399-23	Sequence 23, Appl
22	26.8	9.9	2236	4	US-09-310-367-23	Sequence 23, Appl
23	26.8	9.9	2236	4	US-09-032-337-23	Sequence 23, Appl
24	26.8	9.9	2236	4	US-09-464-231-23	Sequence 23, Appl
25	26.6	9.8	587	4	US-09-833-381-1690	Sequence 1690, Ap
26	26.6	9.8	1317	4	US-09-016-434-1446	Sequence 1446, Ap
27	26.6	9.8	1578	4	US-09-354-138-134	Sequence 134, App

ALIGNMENTS

RESULT 1

US-08-475-891A-3/c

; Sequence 3, Application US/08475891A

; Patent No. 5859339

; GENERAL INFORMATION:

APPLICANT: Ronald, Pamela C.

APPLICANT: Wang, Guo-Liang

APPLICANT: Song, Wen-Yuang

TITLE OF INVENTION: Procedures and Materials for Confering

TITLE OF INVENTION: Disease Resistance in Plants

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475.891A

FILING DATE: 06-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/373,375

FILING DATE: 17-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Bastian, Kevin L.

REGISTRATION NUMBER: 34, 774

REFERENCE/DOCKET NUMBER: 02370-058910US

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 5992 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

- Sequence 281, Appl
- Sequence 1, Appli
- Sequence 1, Appli
- Sequence 1, Appli
- Sequence 1159, Ap
- Sequence 8976, Ap
- Sequence 15, Appl
- Sequence 3, Appli
- Sequence 30, Appli
- Sequence 1, Appli
- Sequence 15, Appl
- Sequence 15, Appl
- Sequence 1, Appli
- Sequence 13, Appli
- Sequence 7, Appli
- Sequence 9, Appli
- Sequence 12, Appli
- Sequence 22, Appli

```
; OTHER INFORMATION: sativa)"
US-08-475-891A-3

Query Match      10.7%; Score 29; DB 2; Length 5992;
Best Local Similarity 67.2%; Pred. No. 2;
Matches 41; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 65 AGGATGAAACGGTCGGTAACTACCGGATTTTCCCATCTTACTT 124
    |||||
Db 5528 AGGATGAAACGGTCGGTAACTACCGGATTTTCCCATCTTACTT 124
    |||||
QY 125 T 125
Db 5468 T 5468

RESULT 2
US-09-252-991A-12771/c
; Sequence 12771, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12771
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12771

Query Match      10.1%; Score 27.4; DB 4; Length 777;
Best Local Similarity 51.2%; Pred. No. 2.6;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 78 GTCGGTAACGGTCGGTAAATACTACCGGATTTTCCCATCTTACTTCCCGGGCTA 137
    |||||
Db 660 GTCGGCTGGTTGGACACGTCACAGGCAAGTTGTCGCCCAATTACAGCCAGGGGCGC 601
    |||||
QY 138 CAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTTGGAGTCGGGTCGGGTC 197
    |||||
Db 600 GACAAACAGCAGATCAACCTCGGAGCAAGCGGTCGGTAGTGTGTCATTCCGGGGGAGTG 541
    |||||
QY 198 AGTT 202
Db 540 ACCTT 536

RESULT 3
US-09-252-991A-13017
; Sequence 13017, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13017
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13017

Query Match      10.1%; Score 27.4; DB 4; Length 1008;
Best Local Similarity 51.2%; Pred. No. 3;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 78 GTCGGTAACGGTCGGTAAATACTACCGGATTTTCCCATCTTACTTCCCGGGCTA 137
    |||||
Db 1939 GTCGGCTGGTTGGACACGTCACAGGCAAGTTGTCGCCCAATTACAGCCAGGGGCGC 1998
    |||||
QY 138 CAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTTGGAGTCGGGTCGGGTC 197
    |||||
Db 1999 GACAAACAGCAGATCAACCTCGGAGCAAGCGGTCGGTAGTGTGTCATTCCGGGGGAGTG 2058
    |||||
QY 198 AGTT 202
Db 2059 ACCTT 2063

RESULT 4
US-09-252-991A-13185
; Sequence 13185, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13185
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13185

Query Match      10.1%; Score 27.4; DB 4; Length 2577;
Best Local Similarity 51.2%; Pred. No. 5.1;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 78 GTCGGTAACGGTCGGTAAATACTACCGGATTTTCCCATCTTACTTCCCGGGCTA 137
    |||||
Db 1939 GTCGGCTGGTTGGACACGTCACAGGCAAGTTGTCGCCCAATTACAGCCAGGGGCGC 1998
    |||||
QY 138 CAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTTGGAGTCGGGTCGGGTC 197
    |||||
Db 1999 GACAAACAGCAGATCAACCTCGGAGCAAGCGGTCGGTAGTGTGTCATTCCGGGGGAGTG 2058
    |||||
QY 198 AGTT 202
Db 2059 ACCTT 2063

RESULT 5
US-09-801-861-3/c
; Sequence 3, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/801,861
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13017
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-801-861-3/c
```

```
; OTHER INFORMATION: sativa)"
US-08-475-891A-3

Query Match      10.7%; Score 29; DB 2; Length 5992;
Best Local Similarity 67.2%; Pred. No. 2;
Matches 41; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 65 AGGATGAAACGGTCGGTAACTACCGGATTTTCCCATCTTACTT 124
    |||||
Db 5528 AGGATGAAACGGTCGGTAACTACCGGATTTTCCCATCTTACTT 124
    |||||
QY 125 T 125
Db 5468 T 5468

RESULT 2
US-09-252-991A-12771/c
; Sequence 12771, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 12771
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12771

Query Match      10.1%; Score 27.4; DB 4; Length 777;
Best Local Similarity 51.2%; Pred. No. 2.6;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 78 GTCGGTAACGGTCGGTAAATACTACCGGATTTTCCCATCTTACTTCCCGGGCTA 137
    |||||
Db 660 GTCGGCTGGTTGGACACGTCACAGGCAAGTTGTCGCCCAATTACAGCCAGGGGCGC 601
    |||||
QY 138 CAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTTGGAGTCGGGTCGGGTC 197
    |||||
Db 600 GACAAACAGCAGATCAACCTCGGAGCAAGCGGTCGGTAGTGTGTCATTCCGGGGGAGTG 541
    |||||
QY 198 AGTT 202
Db 540 ACCTT 536

RESULT 3
US-09-252-991A-13017
; Sequence 13017, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13017
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13017

Query Match      10.1%; Score 27.4; DB 4; Length 1008;
Best Local Similarity 51.2%; Pred. No. 3;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 78 GTCGGTAACGGTCGGTAAATACTACCGGATTTTCCCATCTTACTTCCCGGGCTA 137
    |||||
Db 1939 GTCGGCTGGTTGGACACGTCACAGGCAAGTTGTCGCCCAATTACAGCCAGGGGCGC 1998
    |||||
QY 138 CAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTTGGAGTCGGGTCGGGTC 197
    |||||
Db 1999 GACAAACAGCAGATCAACCTCGGAGCAAGCGGTCGGTAGTGTGTCATTCCGGGGGAGTG 2058
    |||||
QY 198 AGTT 202
Db 2059 ACCTT 2063

RESULT 4
US-09-252-991A-13185
; Sequence 13185, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13185
; LENGTH: 2577
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13185

Query Match      10.1%; Score 27.4; DB 4; Length 2577;
Best Local Similarity 51.2%; Pred. No. 5.1;
Matches 64; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 78 GTCGGTAACGGTCGGTAAATACTACCGGATTTTCCCATCTTACTTCCCGGGCTA 137
    |||||
Db 1939 GTCGGCTGGTTGGACACGTCACAGGCAAGTTGTCGCCCAATTACAGCCAGGGGCGC 1998
    |||||
QY 138 CAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTTGGAGTCGGGTCGGGTC 197
    |||||
Db 1999 GACAAACAGCAGATCAACCTCGGAGCAAGCGGTCGGTAGTGTGTCATTCCGGGGGAGTG 2058
    |||||
QY 198 AGTT 202
Db 2059 ACCTT 2063

RESULT 5
US-09-801-861-3/c
; Sequence 3, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/801,861
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 13017
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-801-861-3/c
```



```
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2128
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-2128

Query Match      10.0%; Score 27; DB 4; Length 1074;
Best Local Similarity 51.2%; Pred. No. 4.4;
Matches 63; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 1 GTAGCAGCATCTCTAACACGCTACCCGTTTACCGGTACCGGTACCGGGTGTGG 60
Db 457 GTAGCAGCATCTCTAACACGCTACCCGTTTACCGGTACCGGTACCGGGTGTGG 516
QY 61 CTACAGCGGATGAAACCGGCTACCGGTACCGGTACCGGTACCGGTACCGGTAC 120
Db 517 TTACAGCAGCATCTCTAACACGCTACCCGTTTACCGGTACCGGTACCGGGTGTGG 576
QY 121 ACT 123
Db 577 AAT 579

RESULT 10
US-09-539-333D-127
; Sequence 127, Application US/09539333D
; Patent No. 6476208
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Essioux, Laurent
; TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
; FILE REFERENCE: GENSET.047AUS
; CURRENT APPLICATION NUMBER: US/09/539,333D
; CURRENT FILING DATE: 2000-03-30
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US 60/126,903
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: US 60/131,971
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/132,065
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: US 60/143,928
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 60/145,915
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: US 60/146,453
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/146,452
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: US 60/162,288
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/416,384
; PRIOR FILING DATE: 1999-10-12
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: Patent.pm
; SEQ ID NO 127
; LENGTH: 3001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1501
; OTHER INFORMATION: 99-25961-376 : polymorphic base T or G
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1502..1520
; OTHER INFORMATION: 99-25961-376.misl, complement
; FEATURE:
; NAME/KEY: misc_binding
```

```
; LOCATION: 1481..1500
; OTHER INFORMATION: 99-25961-376.misl2,
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1854..1873
; OTHER INFORMATION: upstream amplification primer, complement
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1391..1411
; OTHER INFORMATION: downstream amplification primer
; FEATURE:
; NAME/KEY: misc_binding
; LOCATION: 1489..1513
; OTHER INFORMATION: 99-25961-376 probe
US-09-539-333D-127

Query Match      10.0%; Score 27; DB 4; Length 3001;
Best Local Similarity 53.3%; Pred. No. 7.9;
Matches 57; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 134 GCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTTGGAGTGGGTG 193
Db 148 GCTAAAGTCAATGACAGCCTCAGGATCACCCCTTTCTTTTCTTTTCTTTTCTTC 207
QY 194 GGTCAAGGTTATGATCGACCCCGTTATTCTTCCATGGGGTGTGTTGA 240
Db 208 AGTCATATGACGCTCAAGCCACGTTTCTCTAAAGAGCTTGACTGA 254

RESULT 11
US-09-754-250-3/c
; Sequence 3, Application US/09754250
; Patent No. 6376225
; GENERAL INFORMATION:
; APPLICANT: WEI, Ming-Hui et al
; TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN
; TITLE OF INVENTION: PHOSPHODIESTERASE PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001063
; CURRENT APPLICATION NUMBER: US/09/754,250
; CURRENT FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 111282
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) .. (111282)
; OTHER INFORMATION: n = A,T,C or G
US-09-754-250-3

Query Match      10.0%; Score 27; DB 4; Length 111282;
Best Local Similarity 56.0%; Pred. No. 58;
Matches 51; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 98 TACTACGGGATTTTCCCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 157
Db 108219 TCCAAAGGGGGTGTTCCTCTCTCCAGTTCTATTTCCTCCCTCCACCCCA 108160
QY 158 GGGAGCAACAGGATCTATTGTTGGAGTGG 188
Db 108159 GTCTGCAACAGCCCATGGGGAGGACTGG 108129

RESULT 12
US-09-621-976-2813/c
; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
```

T 13
 1-829-525-37/c
 pence 37, Application US/08829525
 ent No. 6084083
 NERAL INFORMATION:
 APPLICANT: Levinson, Douglas A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036/2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/829,525
 FILING DATE: 28-MAR-1997
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/609,583
 FILING DATE: 01-MAR-1996
 APPLICATION NUMBER: US 08/487,748
 FILING DATE: 07-JUN-1995
 APPLICATION NUMBER: US 08/398,633
 FILING DATE: 03-MAR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7853-081
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-869-8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 903 base pairs
 TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-829-525-37

Query Match          9.9%; Score 26.8; DB 3; Length 903;
Best Local Similarity 46.7%; Pred. No. 4.8;
Matches 85; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY      84 AACGGTCGGTAAATACTACGGGATTTTCCCATCTACTTTCCATCCCGGGCTACAAGGC 143
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      380 AACTTCAGGTAAATTTTTCATCAATTCGCTGGGATTTGGATCCGGCAGCAGTAG 321
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      144 TTCCCAAGTCATCCGGAGCAACAGAGATCTATTGTGTGGAGTCGGGTCCGGTCAGGTGA 203
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      320 ATCCCACTGTCTGTAGAGTCACAATCTCTATGGTCAGGACACATCTCCTTTGCGGAAA 261
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      204 TGATGACCCGGGTATTCTTCCATGCGGGTTTCTTCAGAGACCTCTCCACTACTCATGAGC 263
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      260 TCCCAATTAGCCAGTATCTGGATGCCAATAATTCACATCCCTTTTCATCAGTCCCGAGC 201
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY      264 TC 265
      |
Db      200 AC 199

RESULT 14
US-08-609-583A-37/c
; Sequence 37, Application US/08609583A
; Patent No. 6204371
; GENERAL INFORMATION:
; APPLICANT: Levinson, Douglas A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITL OF INVENTION: TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,583A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,748
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/398,633
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 903 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-609-583A-37

```

Mon May 17 08:32:46 2004

us-09-701-023-2.51304.rni

Page 6

Query Match	9.9%;	Score 26.9;	DB 3;	Length 903;
Best Local Similarity	46.7%;	Pred. No. 4.8;		
Matches	85;	Conservative 0;	Mismatches 97;	Indels 0; Gaps 0;

QY	84	AACGGTCGGTAAATACTACGGGATTTTCCCATCTTAC	TTCCATCCCGGGCTACAAGGC	143
Db	380	AAC TTCAGGTTAAATTTTCATCATTCATTATGCC	TGGGATTTGGATCCGGCAGCAGTAG	321
QY	144	TTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGT	TGGAGTCGGGTCCGGTCAGGTTA	203
Db	320	ATCCCACTGTCTGTAGAGTCACATTCCTATGTCAGG	GACACATCTCCTTTGCCGAAA	261
QY	204	TGATCAGCCCGGTATTTCCTCCATGGGGTTTTCTTG	AGACCTCCTCCACTACTCATGAGC	263
Db	260	TCCCCAATTAGCCAGTATCTGGATGTCCAAATAATTC	ATTCATCCCTTTTCATCAGTCCTGAGC	201
QY	264	TC	265	
Db	200	AC	199	

RESULT 15
 US-08-937-399-37/c
 ; Sequence 37, Application US/08937399
 ; Patent No. 6288218
 ; GENERAL INFORMATION:
 ; APPLICANT: Levinson, Douglas A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036/2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/937,399
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/609,583
 ; FILING DATE: 01-MAR-1996
 ; APPLICATION NUMBER: US 08/487,748
 ; FILING DATE: 07-JUN-1995
 ; APPLICATION NUMBER: US 08/398,633
 ; FILING DATE: 03-MAR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-048
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212-790-9090
 ; TELEFAX: 212-869-8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 37:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 903 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 US-08-937-399-37

```
Query Match          9.9%; Score 26.8; DB 3; Length 903;
Best Local Similarity 46.7%; Pred. No. 4.8;
Matches 85; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
```


<hr/>					
; GENERAL INFORMATION:					
; APPLICANT: Dellaporta, Stephen L.					
; APPLICANT: Moreno, Maria A.					
; APPLICANT: Yale University					
; TITLE OF INVENTION: Methods and Compositions to Reduce or Eliminate					
; TITLE OF INVENTION: Transmission of a Transgene					
; FILE REFERENCE: 44574-5078-US					
; CURRENT APPLICATION NUMBER: US/09/794,384A					
; PRIOR FILING DATE: 2001-02-28					
; PRIOR APPLICATION NUMBER: US 60/185,524					
; PRIOR FILING DATE: 2000-02-28					
; NUMBER OF SEQ ID NOS: 16					
; SOFTWARE: Patentin Ver. 2.1					
; SEQ ID NO 3					
; LENGTH: 4565					
; TYPE: DNA					
; ORGANISM: Zea mays					
; FEATURE:					
; OTHER INFORMATION: Transposable element Ac					
US-09-794-384A-3					
Query Match 14.4%; Score 39; DB 9; Length 4565;					
Best Local Similarity 76.2%; Pred.No. 0.0025;					
Matches 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;					
Qy	65	AGGGATGAAACCGTTCGGTAACGGTCGGTAAATACTACGGGATTTCCTCCACTT	124		
Dd	2	AGGGATGAAACCGTTCGGTAACGGTCGGTAAATACTCTACGGTTTCATTTCA	TATT	61	
Qy	125	TCA	127		
Dd	62	TAA	64		
RESULT 3					
US-10-138-221-8/c					
; Sequence 8, Application US/10138221					
; Publication No. US20020199216A1					
; GENERAL INFORMATION:					
; APPLICANT: Amy P. MacRae					
; TITLE OF INVENTION: USE OF TRANSPOSABLE ELEMENTS FOR ALTERING GENE EXPRESSION					
; FILE REFERENCE: 51178/7					
; CURRENT APPLICATION NUMBER: US/10/138,221					
; CURRENT FILING DATE: 2002-08-01					
; PRIOR APPLICATION NUMBER: US 60/287,882					
; PRIOR FILING DATE: 2001-05-01					
; NUMBER OF SEQ ID NOS: 9					
; SOFTWARE: Patentin version 3.1					
; SEQ ID NO 8					
; LENGTH: 4565					
; TYPE: DNA					
; ORGANISM: Zea mays					
US-10-138-221-8					
Query Match 14.4%; Score 39; DB 14; Length 4565;					
Best Local Similarity 76.2%; Pred.No. 0.0025;					
Matches 48; Conservative 0; Mismatches 15; Indels 0; Gaps 0;					
Qy	65	AGGGATGAAACCGTTCGGTAACGGTCGGTAAATACTACGGGATTTCCTCCACTT	124		
Dd	4564	AGGGATGAAACCGTTCGGTAACGGTCGGTAAATACTCTACGGTTTCATTTCA	TATT	4505	
Qy	125	TCA	127		
Dd	4504	TAA	4502		
RESULT 4					
US-10-027-632-213703/c					
; Sequence 213703, Application US/10027632					
; Publication No. US20020198371A1					
; GENERAL INFORMATION:					
; APPLICANT: Wang, David G.					
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide					
; TITLE OF INVENTION: Polymorphisms in the Human Genome					
; FILE REFERENCE: 108827.129					
; CURRENT APPLICATION NUMBER: US/10/027,632					
; CURRENT FILING DATE: 2002-04-30					
; PRIOR APPLICATION NUMBER: US 60/218,006					
; PRIOR FILING DATE: 2000-07-12					
; PRIOR APPLICATION NUMBER: US 60/198,676					
; PRIOR FILING DATE: 2000-04-20					
; PRIOR APPLICATION NUMBER: US 60/193,483					
; PRIOR FILING DATE: 2000-03-29					
; PRIOR APPLICATION NUMBER: US 60/185,218					
; PRIOR FILING DATE: 2000-02-24					
; PRIOR APPLICATION NUMBER: US 60/167,363					
; PRIOR FILING DATE: 1999-11-23					
; PRIOR APPLICATION NUMBER: US 60/156,358					
; PRIOR FILING DATE: 1999-09-28					
; PRIOR APPLICATION NUMBER: US 60/146,002					
; PRIOR FILING DATE: 1999-08-09					
; NUMBER OF SEQ ID NOS: 325720					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 213704					
; LENGTH: 533					
; GENERAL INFORMATION:					
; APPLICANT: Wang, David G.					
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide					
; TITLE OF INVENTION: Polymorphisms in the Human Genome					
; FILE REFERENCE: 108827.129					
; CURRENT APPLICATION NUMBER: US/10/027,632					
; CURRENT FILING DATE: 2002-04-30					
; PRIOR APPLICATION NUMBER: US 60/218,006					
; PRIOR FILING DATE: 2000-07-12					
; PRIOR APPLICATION NUMBER: US 60/198,676					
; PRIOR FILING DATE: 2000-04-20					
; PRIOR APPLICATION NUMBER: US 60/193,483					
; PRIOR FILING DATE: 2000-03-29					
; PRIOR APPLICATION NUMBER: US 60/185,218					
; PRIOR FILING DATE: 2000-02-24					
; PRIOR APPLICATION NUMBER: US 60/167,363					
; PRIOR FILING DATE: 1999-11-23					
; PRIOR APPLICATION NUMBER: US 60/156,358					
; PRIOR FILING DATE: 1999-09-28					
; PRIOR APPLICATION NUMBER: US 60/146,002					
; PRIOR FILING DATE: 1999-08-09					
; NUMBER OF SEQ ID NOS: 325720					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 213704					
; LENGTH: 533					
; GENERAL INFORMATION:					
; APPLICANT: Wang, David G.					
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide					
; TITLE OF INVENTION: Polymorphisms in the Human Genome					
; FILE REFERENCE: 108827.129					
; CURRENT APPLICATION NUMBER: US/10/027,632					
; CURRENT FILING DATE: 2002-04-30					
; PRIOR APPLICATION NUMBER: US 60/218,006					
; PRIOR FILING DATE: 2000-07-12					
; PRIOR APPLICATION NUMBER: US 60/198,676					
; PRIOR FILING DATE: 2000-04-20					
; PRIOR APPLICATION NUMBER: US 60/193,483					
; PRIOR FILING DATE: 2000-03-29					
; PRIOR APPLICATION NUMBER: US 60/185,218					
; PRIOR FILING DATE: 2000-02-24					
; PRIOR APPLICATION NUMBER: US 60/167,363					
; PRIOR FILING DATE: 1999-11-23					
; PRIOR APPLICATION NUMBER: US 60/156,358					
; PRIOR FILING DATE: 1999-09-28					
; PRIOR APPLICATION NUMBER: US 60/146,002					
; PRIOR FILING DATE: 1999-08-09					
; NUMBER OF SEQ ID NOS: 325720					
; SOFTWARE: FastSeq for Windows Version 4.0					
; SEQ ID NO 213704					
; LENGTH: 533					
; GENERAL INFORMATION:					
; APPLICANT: Wang, David G.					
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide					
; TITLE OF					

YPB: DNA
ORGANISM: Human
-027-632-213704

Query Match 12.3%; Score 33.4; DB 13; Length 533;
Best Local Similarity 52.6%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;
125 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 184
126 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 184
336 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 277
337 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 277
185 GTCGGGTCGGGTACAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 244
186 GTCGGGTCGGGTACAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 244
276 ACGGAGAGGAGGAGTATGTTGGCTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 217
245 TCCTCCCACTACTC 257
246 TCCTCCCACTACTC 257
216 CCCTGCCCAATTC 204

T 6

-027-632-213703/c
Sequence 213703, Application US/10027632
Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027.632

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 213703

LENGTH: 533

TYPE: DNA

ORGANISM: Human

-027-632-213703

Query Match 12.3%; Score 33.4; DB 16; Length 533;
Best Local Similarity 52.6%; Pred. No. 0.12; Indels 0; Gaps 0;
Matches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;
125 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 184
126 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 184
336 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 277
337 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 277
185 GTCGGGTCGGGTACAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 244
186 GTCGGGTCGGGTACAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 244
276 ACGGAGAGGAGGAGTATGTTGGCTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 217
245 TCCTCCCACTACTC 257
246 TCCTCCCACTACTC 257
216 CCCTGCCCAATTC 204

T 7,

-027-632-213704/c

Sequence 213704, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027.632

PRIOR FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR FILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 213704

LENGTH: 533

TYPE: DNA

ORGANISM: Human

-10-027-632-213704

Query Match 12.3%; Score 33.4; DB 16; Length 533;

Best Local Similarity 52.6%; Pred. No. 0.12;

Matches 70; Conservative 1; Mismatches 62; Indels 0; Gaps 0;

Qy 125 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 184

Db 336 TCATCCCGGGCTACAAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 277

Qy 185 GTCGGGTCGGGTACAGGCTTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 244

Db 276 ACGGAGAGGAGGAGTATGTTGGCTCCCAAGCTCATCGGAGCAACAGGATCTATTGTGGTGA 217

Qy 245 TCCTCCCACTACTC 257

Db 216 CCCTGCCCAATTC 204

RESULT 8

US-10-425-114-3402/c

Sequence 3402, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Kovalic, David K.

APPLICANT: Screen, Steven E.

APPLICANT: Tabaska, Jack E.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with

Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425.114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 3402

LENGTH: 2360

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

OTHER INFORMATION: Clone ID: 700264066_FLI

US-10-425-114-3402

Query Match	11.9%	Score 32.2;	DB 13;	Length 2360;
Best Local Similarity	70.5%	Pred. No. 0.63;		
Matches	43;	Conservative 0;	Mismatches 18;	Indels 0; Gaps 0;

Qy	65	AGGGATGAAAACGGTTCGGTAAACGGTTCGGTAAAAATATCTACGGGATTTTTCCTACCTT	124
Db	1785	AGGGATGAAAACGGTTCGGTAAACGGTTCGGTAAACCAACCAATACCGGTTTTCATATT	1726
Qy	125	T 125	
Db	1725	T 1725	

```

RESULT 9
US-10-027-632-174961/c
; Sequence 174961, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174961
; LENGTH: 3186778
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(3186778)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-174961

```

	Query Match	11.4%	Score 30.8	DB 13	Length 3186778
	Best Local Similarity	55.7%	Pred. No. 37		
	Matches 59	Conservative 0	Mismatches 47	Indels 0	Gaps 0
QY	16	AACAACGCTACCGTTTACCGTACCGGTAGACCCGGGTGTTGTGCTACAGGATGAAAA	75		
Db	2949368	AATACCACCACCTCGTCTCTTAGAACCGTGGCCACGAGCTTGTTAAAAAGAAATGCTAA	2949309		
QY	76	CGTCCGGTAACGTCGGTAAATACTACGGGATTTTCCATCCTA	121		
Db	2949308	CCGCGCATAGGGTCTCTGAAGATATTACGAAAGGCTTCTCTCCTA	2949263		

RESULT 10
US-10-027-632-174961/c
; Sequence 174961, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632

```

/ CURRENT FILING DATE: 2002-04-30
/ PRIOR APPLICATION NUMBER: US 60/218,006
/ PRIOR FILING DATE: 2000-07-12
/ PRIOR APPLICATION NUMBER: US 60/198,676
/ PRIOR FILING DATE: 2000-04-20
/ PRIOR APPLICATION NUMBER: US 60/193,483
/ PRIOR FILING DATE: 2000-03-29
/ PRIOR APPLICATION NUMBER: US 60/185,218
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: US 60/167,363
/ PRIOR FILING DATE: 1999-11-23
/ PRIOR APPLICATION NUMBER: US 60/156,358
/ PRIOR FILING DATE: 1999-09-28
/ PRIOR APPLICATION NUMBER: US 60/146,002
/ PRIOR FILING DATE: 1999-08-09
/ NUMBER OF SEQ ID NOS: 325720
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 174961
/ LENGTH: 3186778
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)...(3186778)
/ OTHER INFORMATION: n = A,T,C or G
US 10-027-632-174961

```

	Query Match	11.4%	Score 30.8;	DB 16;	Length 3186778;
	Best Local Similarity	55.7%;	Pred. No. 37;		
	Matches	59;	Conservative 0;	Mismatches 47;	Indels 0; Gaps 0;
Qy	16	AAACAACGCTACCGTTTACCGGTACCGGTAGACCCGGGTGTTGTGTACGGGATGAAAA	75		
Db	2949368	AATACCAACCACCTCGTCTCTTAGGAACGGTGGCCACCAGCGCTTGTAAAAAAGAATGCTAA	2949309		
Qy	76	CGGTGCGGTACGTCGGTAAATACTACGGGATTTTCCCATCCTA	121		
Db	2949308	CGGCGCATAGGGTCTCGAAGATATTACGAAAGGGTTCTCTCCTA	2949263		

```

RESULT 11
US-10-106-698-1963/c
; Sequence 1963, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patent In Ver. 3.0
; SEQ ID NO 1963
; LENGTH: 1022
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-106-698-1963

```

	Query Match	11.1%	Score 30.2	DB 15	Length 1022
	Best Local Similarity	51.9%	Pred. No. 2.5		
	Matches 68	Conservative 0	Mismatches 63	Indels 0	Gaps 0
Qy	33	ACCGGTACCGGTAGACCGGGTGTGTGCTACAGGATGAAACGGTCCGTAAACGGTCGG	92		
Db	411	ACACGAATAGTTGACACCGCGCTCCAGGAGGTGCAAGAGACGGGTGTTCCACATCGA	352		
Qy	93	TAAATACTACGGGATTTTTTCCCATCTACTTTTCATCCGGGGTACAAGGGTTCCTCCCAAGC	152		

351 TCAGTACTTGGGCGCCCTCCCGTTACCTTGTAAATCCGGACACACGTGCGTCCCGTTGT 292
153 TCATCGGAGC 163
291 GCATCTGCCGC 281

AT 12
-006-285-506/c
ence 506, Application US/10006285
lication No. US20030165854A1
ERAL INFORMATION:
PLICANT: Mary Jane Cunningham
PLICANT: Matthew R. Kaser
LE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
LE REFERENCE: PA-0039 US
RRENT APPLICATION NUMBER: US/10/006,285
RRENT FILING DATE: 2001-12-05
MBER OF SEQ ID NOS: 514
FTWARE: PERL Program
ID NO 506
LENGTH: 1759
YPE: DNA
RGANISM: Homo sapiens
EATURE:
AME/KEY: misc feature
THER INFORMATION: Incyte ID No. US20030165854A1 235106.13
AME/KEY: unsure
OCATION: 1183-1314, 1485-1577
THER INFORMATION: a, t, c, g, or other
-006-285-506

ary Match 11.1%; Score 30.2; DB 15; Length 1759;
t Local Similarity 51.9%; Pred. No. 3.1;
ches 68; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

33 ACCGTACCGGTACACCGCGTGTGTGCTACAGGATGAACGGTCGTAACGGTCGG 92
815 ACACGAATAGTTGACCACCGCGTCCAGGAGGTGCAAGAGACGGTGTTCACATCGA 756
93 TAAATACTACGGGATTTTCCCATCTCTATCTTCATCCCGGGCTACAGGCTTCCCAAGC 152
755 TCAGTACTTGGGCGCCCTCCCGTTCACCTTGTAAATCCGGACACACGTGCGTCCCGTTGT 696
153 TCATCGGAGC 163
695 GCATCTGCCGC 685

AT 13
-087-192-451
ence 451, Application US/10087192
lication No. US20020182586A1
ERAL INFORMATION:
PLICANT: Morris, David W.
PLICANT: Engelhard, Eric K.
LE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TLE OF INVENTION: CANCER
LE REFERENCE: 529452000122
RRENT APPLICATION NUMBER: US/10/087,192
RRENT FILING DATE: 2002-03-01
ROR APPLICATION NUMBER: US 09/747,377
ROR FILING DATE: 2000-12-22
ROR APPLICATION NUMBER: US 09/798,586
ROR FILING DATE: 2001-03-02
MBER OF SEQ ID NOS: 2059
FTWARE: FastSeq for Windows Version 4.0
ID NO 451
LENGTH: 256525
YPE: DNA
RGANISM: Mus musculus
EATURE:

; NAME/KEY: misc feature
; LOCATION: (1)...(256525)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-451

Query Match 10.9%; Score 29.6; DB 13; Length 256525;
Best Local Similarity 59.5%; Pred. No. 38;
Matches 50; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 106 GATTTTCCCATCTCTACTTTTCATCCCGGGCTACAGGCTTCCCAAGCTCATCGGAGCAA 165
DB 106805 GCTTTTCCCATCTCTACTTTCCCATCTCCCATCTCCATGTTTCAAACTAGTCTGGGCTT 106864

QY 166 CAGGATCTATTGTGTGGAGTCGG 189
DB 106865 TAGCGCTAGCATTTGTGAAGATCG 106888

RESULT 14
US-09-919-497-18
Sequence 18, Application US/09919497
Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REFERENCE: B0801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn version 3.0
SEQ ID NO 18
LENGTH: 6746
TYPE: DNA
ORGANISM: Homo sapiens
US-09-919-497-18

Query Match 10.8%; Score 29.4; DB 9; Length 6746;
Best Local Similarity 55.3%; Pred. No. 10;
Matches 57; Conservative 0; Mismatches 46; Indels 0; Gaps 0;

QY 98 TACTACGGGATTTTCCCATCTCTACTTTTCATCCCGGGCTACAGGCTTCCCAAGCTCATC 157
DB 1928 TACTAGGGGTTTCTCCCTCCATCGGCACATCCAGGATCCCTGGCAGCTGCTGGCCTCC 1987

QY 158 GCGAGCAACAGGATCTATTGTGTGGAGTCGGTGGGTGAGG 200
DB 1988 AGCAACCCCATCTTAGTTGTGTGGAGTGGGTTGTGGCATG 2030

RESULT 15
US-09-967-768A-303
Sequence 303, Application US/09967768A
Patent No. US20020150877A1
GENERAL INFORMATION:
APPLICANT: Augustus, Meena
TITLE OF INVENTION: Cancer
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-72
CURRENT APPLICATION NUMBER: US/09/967,768A
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US/60/236,109
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,034
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236,111
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 325
SOFTWARE: PatentIn version 3.0
SEQ ID NO 303
LENGTH: 6746
TYPE: DNA

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

iclcic - nucleic search, using sw model

rn: May 16, 2004, 12:37:50 ; Search time 3198 Seconds
(without alignments)
2530.535 Million cell updates/sec

ct score: 271
US-09-701-023-2
1 gtagcatgctctcttaaa.....ctactcatgagctctcttca 271

ng table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

hed: 27513289 seqs, 14931090276 residues
number of hits satisfying chosen parameters: 55026578

hum DB seq length: 0
num DB seq length: 2000000000

processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

base : EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpi.*
7: em_estro.*
8: em_htc.*
9: gb_est1.*
10: gb_est2.*
11: gb_htc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_pbg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

CF331338 NACL--07-
CF331337 NACL--07-
CF330495 NACL--06-
CG734690 ZMMBB029
CG171886 PUFME37TD
CG171885 PUFME37TB
CC371520 PUHBB30TB
CD435731 EL01NG365
CC623062 CGWHB66TV
CC371523 PUHBB30TD
CG873669 ZMMBB028
CG420254 ZMMBB003
BZ788279 PUGDX08TB
BH782423 fmb011f0
CG409347 Ds1043 Ds
CG322358 OG0BS14TV
CD972576 OAE23e03.
CC026132 3591.1.4
CC66071 CGWHB64TH
CG737340 ZMMBB032
CG435797 OG5D035TC
CC350259 OGPAF79TV
BZ665854 SGT1516-3
CG782485 1123050F0
BZ812754 PUGBX29TD
BZ812750 PUGBX29TB
CC706884 OGUGR86TH
CG254695 OGVC072TV
BH442449 BB442449
BZ665884 SGT1742-3
CG738843 ZMMBB018
BH779656 fmb014f0
CD974521 QAE47B09.
CE712344 tigr-g88-
BZ751811 PUFBX58TD
CC715778 OGUPH48TH
BZ665942 SGT2837-3
BZ960565 PUGGI67TD
CC879337 ZMMBB021
CF788439 860390 MA

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

nucleic - nucleic search, using sw model

run:      May 16, 2004, 12:37:50 ; Search time 3198 Seconds
        (without alignments)
        2530.535 Million cell updates/sec

::
fact score: 271
source: 1 gcagcatgatcttaacaa.....ctactcatgagctctcttca 271

index table: IDENTITY NUC
            Gapop 10.0 , Gapext 1.0

aligned: 27513289 seqs, 14931090276 residues

        number of hits satisfying chosen parameters: 55026578

num DB seq length: 0
num DB seq length: 2000000000

processing: Minimum Match 0%
            Maximum Match 100%
            Listing first 45 summaries

base :
      1: em_estba.*
      2: em_esthum.*
      3: em_estin.*
      4: em_estmu.*
      5: em_estov.*
      6: em_estpl.*
      7: em_estro.*
      8: em_htc.*
      9: gb_est1.*
     10: gb_est2.*
     11: gb_htc.*

```

ALIGNMENTS

RESULT 1
BH472044/c
LOCUS
DEFINITION BH472044 BOHU Brassica oleracea genomic clone BOHUA43, genomic survey sequence.
ACCESSION BH472044
VERSION BH472044.1 GI:17680155
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 641)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
Other_GSSs: BOHUA43TF
Contact: Chris Town
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

It	Score	Query Match	Length	DB ID	Description
1	55.8	20.6	641	28	BH472044 BOHUA43TR
2	55.4	20.4	554	28	BZ471957 BONNK77TR
3	40.2	14.8	214	28	AZ923008 OsAc4-1 P
4	39	14.4	282	29	CG409294 Ds990 Ds

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

```

FEATURES
  source
    Location/Qualifiers
      1..641
        /organism="Brassica oleracea"
        /mol_type="genomic DNA"
        /strain="TO1000DH3"
        /db_xref="taxon:3712"
        /clone="BOHUA43"
        /note="Vector: pHO51; Site 1: BatXI; 2-3 kb sheared
        genomic DNA inserted into pHO51 using BstXI linkers"
ORIGIN
  Query Match      20.6%; Score 55.8; DB 28; Length 641;
  Best Local Similarity 75.2%; Pred. No. 7e-07;
  Matches 85; Conservative 0; Mismatches 22; Indels 6; Gaps 1;
QY 159 GGAGCAAGGATCTATTGCTGGAGTCGGGTCCGGTCAGGTTATGATCGACCCGGTTA 218
DB 302 GAAGCAGGTTCTTTCCGGGGAGGAGCGCGGTCCGGTCAGATCATGATAGACCGGTTT 243
QY 219 TTCTTCATGGGTTTGTGTGAGACCTCTCCACTACTCATGAGCTCTCTTCA 271
DB 242 GTTCTCTGGGTTTGTGAGACATCC-----ACTCATGAGCTCTCTTCA 196

RESULT 2
LOCUS      BZ471957      554 bp      DNA      linear      GSS 13-DEC-2002
DEFINITION BONNK77R BO.1.6.2_KB_tot Brassica oleracea genomic clone BONNK77,
            genomic survey sequence.
ACCESSION  BZ471957
VERSION    BZ471957.1 GI:26770554
KEYWORDS
SOURCE
  ORGANISM
    Brassica oleracea
    Brassica oleracea
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
  1 (bases 1 to 554)
  Town,C.D., Van Axen,S., Utterback,T., Koo,H. and Fraser,C.M.
  Whole genome shotgun sequencing of Brassica oleracea
  Unpublished (2001)
  Other GSSs: BONNK77F
  Contact: Chris Town
  TIGR
  9712 Medical Center Drive, Rockville, MD 20850, USA.
  Tel: 301-838-3523
  Fax: 301-838-0208
  Email: cdtown@tigr.org
  DNA is from a doubled haploid provided by Tom Osborn.
  Seq primer: TR
  Class: sheared ends.
  Location/Qualifiers
    1..554
      /organism="Brassica oleracea"
      /mol_type="genomic DNA"
      /strain="TO1000DH3"
      /db_xref="taxon:3712"
      /clone="BONNK77"
      /clone_lib="BO.1.6.2_KB_tot"
      /note="Vector: pHO51; Site 1: BatXI; 1.6-2 kb sheared
      total DNA inserted into pHO51 using BstXI linkers"
ORIGIN
  Query Match      20.4%; Score 55.4; DB 28; Length 554;
  Best Local Similarity 82.1%; Pred. No. 9e-07;
  Matches 78; Conservative 0; Mismatches 11; Indels 6; Gaps 1;
QY 177 GTGGTGGAGTCGGGTCCGGTCAGGTTATGATCGACCCGGTTATTTCTCCATGGGTTTG 236
DB 16 GGGGAGGAGCGGGTCGGGTCCAGATCATGATAGACCCGGTTGTTCTCTCTGGGGTTTG 75
QY 237 TTGAGACCTCTCCACTACTCATGAGCTCTCTTCA 271

FEATURES
  source
    Location/Qualifiers
      1..214
        /organism="Oryza sativa (japonica cultivar-group)"
        /mol_type="genomic DNA"
        /cultivar="Nipponbare"
        /db_xref="taxon:39947"
        /clone="2A-8 A"
        /clone_lib="PCR product directly amplified from genomic
        DNA"
ORIGIN
  Query Match      14.8%; Score 40.2; DB 28; Length 214;
  Best Local Similarity 73.9%; Pred. No. 0.056;
  Matches 51; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 59 TGCTACAGGGATGAAAACGGTCGGTAACGGTCGGTAAATACTACGGGATTTTCCCATC 118
DB 3 TGCCTAGGATGAAAACGGTCGGTAACGGTCGGTAAATACTACCTACCGTTTTCATTT 62
QY 119 CTACTTTCA 127
DB 63 CATATTTAA 71

RESULT 4
LOCUS      CG409294      282 bp      DNA      linear      GSS 03-SEP-2003
DEFINITION Ds990 Ds insertion lines Oryza sativa (japonica cultivar-group)
            genomic, genomic survey sequence.
ACCESSION  CG409294
VERSION    CG409294.1 GI:34430659
KEYWORDS
SOURCE
  ORGANISM
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  282 bp
  Ds990 Ds insertion lines Oryza sativa (japonica cultivar-group)
  genomic, genomic survey sequence.
  CG409294.1 GI:34430659
  GSS.
  Oryza sativa (japonica cultivar-group)
  Oryza sativa (japonica cultivar-group)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Ehrhartoideae; Oryzaceae; Oryza.

```

```

Db 76 ATGAGATCC-----ACTCATGAGCTCTCTTCA 104

RESULT 3
LOCUS      AZ923008      214 bp      DNA      linear      GSS 22-MAR-2001
DEFINITION OSAc4-1 PCR product directly amplified from genomic DNA Oryza
            sativa (japonica cultivar-group) genomic clone 2A-8 A, genomic
            survey sequence.
ACCESSION  AZ923008
VERSION    AZ923008.1 GI:13433229
KEYWORDS
SOURCE
  ORGANISM
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.
  1 (bases 1 to 214)
  Greco,R., Ouwkerk,P.B.F., Taal,A.J.C., Favalli,C.,
  Bequiritstain,T., Puigdomenech,P., Colombo,L., Hoge,J.H.C. and
  Pereira,A.
  Early and multiple Ac transposition in rice suitable for efficient
  insertional mutagenesis
  Plant Mol. Biol. (2001) In press
  Contact: Pereira A
  Business Unit Genomics
  Plant Research International
  P.O. Box 16, 6700 AA, Wageningen, The Netherlands
  Tel: 31 317 477114
  Fax: 31 317 418094
  Email: a.pereira@plant.wag-ur.nl
  AC is inserted 5' of this sequence
  Insert Length: 214 Std Error: 0.00
  Class: transposon-tagged
  High quality sequence stop: 214.
  Location/Qualifiers
    1..214
      /organism="Oryza sativa (japonica cultivar-group)"
      /mol_type="genomic DNA"
      /cultivar="Nipponbare"
      /db_xref="taxon:39947"
      /clone="2A-8 A"
      /clone_lib="PCR product directly amplified from genomic
      DNA"
ORIGIN
  Query Match      14.8%; Score 40.2; DB 28; Length 214;
  Best Local Similarity 73.9%; Pred. No. 0.056;
  Matches 51; Conservative 0; Mismatches 18; Indels 0; Gaps 0;
QY 59 TGCTACAGGGATGAAAACGGTCGGTAACGGTCGGTAAATACTACGGGATTTTCCCATC 118
DB 3 TGCCTAGGATGAAAACGGTCGGTAACGGTCGGTAAATACTACCTACCGTTTTCATTT 62
QY 119 CTACTTTCA 127
DB 63 CATATTTAA 71

RESULT 4
LOCUS      CG409294      282 bp      DNA      linear      GSS 03-SEP-2003
DEFINITION Ds990 Ds insertion lines Oryza sativa (japonica cultivar-group)
            genomic, genomic survey sequence.
ACCESSION  CG409294
VERSION    CG409294.1 GI:34430659
KEYWORDS
SOURCE
  ORGANISM
    Oryza sativa (japonica cultivar-group)
    Oryza sativa (japonica cultivar-group)
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
    Ehrhartoideae; Oryzaceae; Oryza.

```

```

1 (bases 1 to 282)
Kim,C.M., Piao,H.L., Park,S.J., Chon,N.S., Je,B.I., Sun,B.,
Park,S.H., Park,J.Y., Lee,E.J., Kim,M.J., Lee,J.J., Nam,M.H.,
Eun,M.Y. and Han,C.D.
Large-scale generation of Ds transposon lines and analysis
of Ds loci in rice
Unpublished (2003)
Contact: Chang-deok Han
Division of Applied Life Science, PMBBRC
Gyeongang National University
Gazwa-dong 900, Jinju 660-701, South Korea
Tel: +82 55 751 6029
Fax: +82 55 759 9363
Email: cdhan@nongae.gsnu.ac.kr
Location: chromosome 10 clone OSJNBa0035F15
Class: transposon-tagged.
Location/Qualifiers
1..282
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Dongjin"
/db_xref="taxon:39947"
/clone_lib="Ds insertion lines"
15 TCA TGT
16 TCA TGT
17 TCA TGT
18 TCA TGT
19 TCA TGT
20 TCA TGT
21 TCA TGT
22 TCA TGT
23 TCA TGT
24 TCA TGT
25 TCA TGT
26 TCA TGT
27 TCA TGT
28 TCA TGT
29 TCA TGT
30 TCA TGT
31 TCA TGT
32 TCA TGT
33 TCA TGT
34 TCA TGT
35 TCA TGT
36 TCA TGT
37 TCA TGT
38 TCA TGT
39 TCA TGT
40 TCA TGT
41 TCA TGT
42 TCA TGT
43 TCA TGT
44 TCA TGT
45 TCA TGT
46 TCA TGT
47 TCA TGT
48 TCA TGT
49 TCA TGT
50 TCA TGT
51 TCA TGT
52 TCA TGT
53 TCA TGT
54 TCA TGT
55 TCA TGT
56 TCA TGT
57 TCA TGT
58 TCA TGT
59 TCA TGT
60 TCA TGT
61 TCA TGT
62 TCA TGT
63 TCA TGT
64 TCA TGT
65 TCA TGT
66 TCA TGT
67 TCA TGT
68 TCA TGT
69 TCA TGT
70 TCA TGT
71 TCA TGT
72 TCA TGT
73 TCA TGT
74 TCA TGT
75 TCA TGT
76 TCA TGT
77 TCA TGT
78 TCA TGT
79 TCA TGT
80 TCA TGT
81 TCA TGT
82 TCA TGT
83 TCA TGT
84 TCA TGT
85 TCA TGT
86 TCA TGT
87 TCA TGT
88 TCA TGT
89 TCA TGT
90 TCA TGT
91 TCA TGT
92 TCA TGT
93 TCA TGT
94 TCA TGT
95 TCA TGT
96 TCA TGT
97 TCA TGT
98 TCA TGT
99 TCA TGT
100 TCA TGT
101 TCA TGT
102 TCA TGT
103 TCA TGT
104 TCA TGT
105 TCA TGT
106 TCA TGT
107 TCA TGT
108 TCA TGT
109 TCA TGT
110 TCA TGT
111 TCA TGT
112 TCA TGT
113 TCA TGT
114 TCA TGT
115 TCA TGT
116 TCA TGT
117 TCA TGT
118 TCA TGT
119 TCA TGT
120 TCA TGT
121 TCA TGT
122 TCA TGT
123 TCA TGT
124 TCA TGT
125 TCA TGT
126 TCA TGT
127 TCA TGT
128 TCA TGT
129 TCA TGT
130 TCA TGT
131 TCA TGT
132 TCA TGT
133 TCA TGT
134 TCA TGT
135 TCA TGT
136 TCA TGT
137 TCA TGT
138 TCA TGT
139 TCA TGT
140 TCA TGT
141 TCA TGT
142 TCA TGT
143 TCA TGT
144 TCA TGT
145 TCA TGT
146 TCA TGT
147 TCA TGT
148 TCA TGT
149 TCA TGT
150 TCA TGT
151 TCA TGT
152 TCA TGT
153 TCA TGT
154 TCA TGT
155 TCA TGT
156 TCA TGT
157 TCA TGT
158 TCA TGT
159 TCA TGT
160 TCA TGT
161 TCA TGT
162 TCA TGT
163 TCA TGT
164 TCA TGT
165 TCA TGT
166 TCA TGT
167 TCA TGT
168 TCA TGT
169 TCA TGT
170 TCA TGT
171 TCA TGT
172 TCA TGT
173 TCA TGT
174 TCA TGT
175 TCA TGT
176 TCA TGT
177 TCA TGT
178 TCA TGT
179 TCA TGT
180 TCA TGT
181 TCA TGT
182 TCA TGT
183 TCA TGT
184 TCA TGT
185 TCA TGT
186 TCA TGT
187 TCA TGT
188 TCA TGT
189 TCA TGT
190 TCA TGT
191 TCA TGT
192 TCA TGT
193 TCA TGT
194 TCA TGT
195 TCA TGT
196 TCA TGT
197 TCA TGT
198 TCA TGT
199 TCA TGT
200 TCA TGT
201 TCA TGT
202 TCA TGT
203 TCA TGT
204 TCA TGT
205 TCA TGT
206 TCA TGT
207 TCA TGT
208 TCA TGT
209 TCA TGT
210 TCA TGT
211 TCA TGT
212 TCA TGT
213 TCA TGT
214 TCA TGT
215 TCA TGT
216 TCA TGT
217 TCA TGT
218 TCA TGT
219 TCA TGT
220 TCA TGT
221 TCA TGT
222 TCA TGT
223 TCA TGT
224 TCA TGT
225 TCA TGT
226 TCA TGT
227 TCA TGT
228 TCA TGT
229 TCA TGT
230 TCA TGT
231 TCA TGT
232 TCA TGT
233 TCA TGT
234 TCA TGT
235 TCA TGT
236 TCA TGT
237 TCA TGT
238 TCA TGT
239 TCA TGT
240 TCA TGT
241 TCA TGT
242 TCA TGT
243 TCA TGT
244 TCA TGT
245 TCA TGT
246 TCA TGT
247 TCA TGT
248 TCA TGT
249 TCA TGT
250 TCA TGT
251 TCA TGT
252 TCA TGT
253 TCA TGT
254 TCA TGT
255 TCA TGT
256 TCA TGT
257 TCA TGT
258 TCA TGT
259 TCA TGT
260 TCA TGT
261 TCA TGT
262 TCA TGT
263 TCA TGT
264 TCA TGT
265 TCA TGT
266 TCA TGT
267 TCA TGT
268 TCA TGT
269 TCA TGT
270 TCA TGT
271 TCA TGT
272 TCA TGT
273 TCA TGT
274 TCA TGT
275 TCA TGT
276 TCA TGT
277 TCA TGT
278 TCA TGT
279 TCA TGT
280 TCA TGT
281 TCA TGT
282 TCA TGT
283 TCA TGT
284 TCA TGT
285 TCA TGT
286 TCA TGT
287 TCA TGT
288 TCA TGT
289 TCA TGT
290 TCA TGT
291 TCA TGT
292 TCA TGT
293 TCA TGT
294 TCA TGT
295 TCA TGT
296 TCA TGT
297 TCA TGT
298 TCA TGT
299 TCA TGT
300 TCA TGT
301 TCA TGT
302 TCA TGT
303 TCA TGT
304 TCA TGT
305 TCA TGT
306 TCA TGT
307 TCA TGT
308 TCA TGT
309 TCA TGT
310 TCA TGT
311 TCA TGT
312 TCA TGT
313 TCA TGT
314 TCA TGT
315 TCA TGT
316 TCA TGT
317 TCA TGT
318 TCA TGT
319 TCA TGT
320 TCA TGT
321 TCA TGT
322 TCA TGT
323 TCA TGT
324 TCA TGT
325 TCA TGT
326 TCA TGT
327 TCA TGT
328 TCA TGT
329 TCA TGT
330 TCA TGT
331 TCA TGT
332 TCA TGT
333 TCA TGT
334 TCA TGT
335 TCA TGT
336 TCA TGT
337 TCA TGT
338 TCA TGT
339 TCA TGT
340 TCA TGT
341 TCA TGT
342 TCA TGT
343 TCA TGT
344 TCA TGT
345 TCA TGT
346 TCA TGT
347 TCA TGT
348 TCA TGT
349 TCA TGT
350 TCA TGT
351 TCA TGT
352 TCA TGT
353 TCA TGT
354 TCA TGT
355 TCA TGT
356 TCA TGT
357 TCA TGT
358 TCA TGT
359 TCA TGT
360 TCA TGT
361 TCA TGT
362 TCA TGT
363 TCA TGT
364 TCA TGT
365 TCA TGT
366 TCA TGT
367 TCA TGT
368 TCA TGT
369 TCA TGT
370 TCA TGT
371 TCA TGT
372 TCA TGT
373 TCA TGT
374 TCA TGT
375 TCA TGT
376 TCA TGT
377 TCA TGT
378 TCA TGT
379 TCA TGT
380 TCA TGT
381 TCA TGT
382 TCA TGT
383 TCA TGT
384 TCA TGT
385 TCA TGT
386 TCA TGT
387 TCA TGT
388 TCA TGT
389 TCA TGT
390 TCA TGT
391 TCA TGT
392 TCA TGT
393 TCA TGT
394 TCA TGT
395 TCA TGT
396 TCA TGT
397 TCA TGT
398 TCA TGT
399 TCA TGT
400 TCA TGT
401 TCA TGT
402 TCA TGT
403 TCA TGT
404 TCA TGT
405 TCA TGT
406 TCA TGT
407 TCA TGT
408 TCA TGT
409 TCA TGT
410 TCA TGT
411 TCA TGT
412 TCA TGT
413 TCA TGT
414 TCA TGT
415 TCA TGT
416 TCA TGT
417 TCA TGT
418 TCA TGT
419 TCA TGT
420 TCA TGT
421 TCA TGT
422 TCA TGT
423 TCA TGT
424 TCA TGT
425 TCA TGT
426 TCA TGT
427 TCA TGT
428 TCA TGT
429 TCA TGT
430 TCA TGT
431 TCA TGT
432 TCA TGT
433 TCA TGT
434 TCA TGT
435 TCA TGT
436 TCA TGT
437 TCA TGT
438 TCA TGT
439 TCA TGT
440 TCA TGT
441 TCA TGT
442 TCA TGT
443 TCA TGT
444 TCA TGT
445 TCA TGT
446 TCA TGT
447 TCA TGT
448 TCA TGT
449 TCA TGT
450 TCA TGT
451 TCA TGT
452 TCA TGT
453 TCA TGT
454 TCA TGT
455 TCA TGT
456 TCA TGT
457 TCA TGT
458 TCA TGT
459 TCA TGT
460 TCA TGT
461 TCA TGT
462 TCA TGT
463 TCA TGT
464 TCA TGT
465 TCA TGT
466 TCA TGT
467 TCA TGT
468 TCA TGT
469 TCA TGT
470 TCA TGT
471 TCA TGT
472 TCA TGT
473 TCA TGT
474 TCA TGT
475 TCA TGT
476 TCA TGT
477 TCA TGT
478 TCA TGT
479 TCA TGT
480 TCA TGT
481 TCA TGT
482 TCA TGT
483 TCA TGT
484 TCA TGT
485 TCA TGT
486 TCA TGT
487 TCA TGT
488 TCA TGT
489 TCA TGT
490 TCA TGT
491 TCA TGT
492 TCA TGT
493 TCA TGT
494 TCA TGT
495 TCA TGT
496 TCA TGT
497 TCA TGT
498 TCA TGT
499 TCA TGT
5
```

RESULT 7

CF330495
 LOCUS NACL--06-D19.bi Rice callus plasmid cDNA library EST 18-AUG-2003
 DEFINITION NACL--06-D19.bi Rice callus plasmid cDNA library (NACL) Oryza
 sativa cDNA clone NACL--06-D19, mRNA sequence.
 ACCESSION CF330495
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1 (bases 1 to 601)
 Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
 Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
 Large-scale Sequencing Analysis of Rice ESTs
 Unpublished (2003)

COMMENT

Contact: Nahm B.H.
 Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
 of Bioscience and Bioinformatics, Myongji University
 Yongin, Kyeonggi, Korea
 Tel: 82 31 330 6193
 Fax: 82 31 321 6355
 Email: bhnahm@gbio.com, bhnahm@bio.myongji.ac.kr.

FEATURES

source
 1..601
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /cultivar="Nackdong"
 /db_xref="taxon:4530"
 /clone="NACL--06-D19"
 /cissue_type="callus"
 /dev_stage="proliferated callus on 2N6 media for 30 days"
 /lab_host="E.coli DH10B"
 /clone_lib="Rice callus plasmid cDNA library (NACL)"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; mRNA was capped
 with oligoribonucleotides and then used as templates for
 RT-PCR."

ORIGIN

Query Match 14.4%; Score 39; DB 14; Length 601;
 Best Local Similarity 76.2%; Pred. No. 0.19; Mismatches 15; Indels 0; Gaps 0;
 Matches 48; Conservative 0;

QY 65 AGGATGAAACGGTCGGTAACGGTCGGTAATAATCTACGGGATTTTCCCATCTACTT 124
 |||||
 DB 2 AGGATGAAACGGTCGGTAACGGTCGGTAATAATCTACGGTTCATTTTCATATT 61
 |||||

QY 125 TCA 127
 ||
 DB 62 TAA 64

RESULT 8

CG734690/c
 LOCUS ZMWBb0290B02.f ZMWBb Zea mays subsp. mays genomic clone
 DEFINITION ZMWBb0290B02 5', genomic survey sequence.
 ACCESSION CG734690
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

CG734690 746 bp DNA linear GSS 22-OCT-2003
 ZMWBb0290B02 5', genomic survey sequence.
 CG734690
 GSS.
 Zea mays subsp. mays (maize)
 Zea mays subsp. mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 746)
 Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
 and Wing,R.

REFERENCE

Sequencing of the maize genome
 Unpublished (2003)
 Contact: Rod Wing

AUTHORS

source
 1..934
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"

Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu

PCR Primers

FORWARD: T7

BACKWARD: M13r

Plate: 0290 row: B column: 02

Seq primer: T7

Class: BAC ends.

FEATURES

source
 1..746
 /organism="Zea mays subsp. mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /sub_species="mays"
 /db_xref="taxon:4578"
 /clone="ZMWBb0290B02"
 /lab_host="DH10B"
 /clone_lib="ZMWBb"
 /note="Vector: pBelOBAC11; Site 1: HindIII; Site 2:
 HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 14.0%; Score 38; DB 29; Length 746;
 Best Local Similarity 75.8%; Pred. No. 0.42;
 Matches 47; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 65 AGGATGAAACGGTCGGTAACGGTCGGTAATAATCTACGGGATTTTCCCATCTACTT 124
 |||||
 DB 302 AGGATGAAACGGTCGGTAACGGTCGGTAATAATCTCTACCATTTTTCATATT 243
 |||||

QY 125 TC 126
 ||

DB 242 TC 241

RESULT 9

CG171886
 LOCUS PUFMF37TD ZM 0.6.1.0.XB Zea mays genomic clone ZMWBra0682G02,
 DEFINITION genomic survey sequence.
 ACCESSION CG171886
 VERSION CG171886.1 GI:34062684
 KEYWORDS GSS.

SOURCE

Zea mays
 Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 934)
 Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
 Bennetzen,J.
 Maize Genomics Consortium
 Unpublished (2003)
 Other_GSSs: PUFMF37TB
 Contact: Cathy Whitelaw
 TIGR

REFERENCE

9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq primer: T7
 Class: sheared ends.

AUTHORS

source
 1..934
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"

TITLE

JOURNAL

COMMENT

/db_xref="taxon:4577"
/clone="ZMMBTa0682G02"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"

try Match 13.9%; Score 37.6; DB 29; Length 934;
st Local Similarity 63.0%; Pred. No. 0.62;
ches 58; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

36 CGTACCGGTAGACCGGGTGTGTGCTACAGGATGAAGCGTTCGTAACGGTCGGTAA 95
716 CGTTGTTGCTGGCTGGCTGCTACCGGTAGGATGAAGCGTTCGTAACGGTCGGTAA 775

96 AATACTACGGGATTTTCCCATCTACTTTCA 127
776 AATACTCTACCGTTTCATTTTCATATTAA 807

AT 10
805/c
ITION PUFMF37TB ZM_0.6_1.0_KB DNA linear GSS 21-AUG-2003
genomic survey sequence.
SION CG171885
RDS GSS.
E Zea mays
ANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 991)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFMF37TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..991
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa0682G02"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"

try Match 13.9%; Score 37.6; DB 29; Length 931;
st Local Similarity 63.0%; Pred. No. 0.62;
ches 58; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

36 CGTACCGGTAGACCGGGTGTGTGCTACAGGATGAAGCGTTCGTAACGGTCGGTAA 95
329 CGTTGTTGCTGGCTGGCTGCTACCGGTAGGATGAAGCGTTCGTAACGGTCGGTAA 270

96 AATACTACGGGATTTTCCCATCTACTTTCA 127
269 AATACTCTACCGTTTCATTTTCATATTAA 238

RESULT 11
CC371520 309 bp DNA linear GSS 19-MAY-2003
LOCUS PUBH230TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa416F12,
DEFINITION genomic survey sequence.
ACCESSION CC371520.1 GI:30845137
VERSION CC371520
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 309)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUBH230TD
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..309
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa416F12"
/clone_lib="ZM_0.6_1.0_KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"

Query Match 13.8%; Score 37.4; DB 28; Length 309;
Best Local Similarity 74.6%; Pred. No. 0.5;
Matches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 65 AGGATGAAAACGGTCGGTAACGGTCGGTAAATACCTACCGGATTTTCCCATCTACTT 124
Db 158 AGGATGAAAACGGTCGGTAACGGTCGGTAAATACCTACCTTACCGTTTTCATATT 217
Qy 125 TCA 127
Db 218 TAA 220

RESULT 12
BZ666626 494 bp DNA linear GSS 03-FEB-2003
LOCUS SGT751-3-3 Arabidopsis thaliana Ds insertion lines Arabidopsis
DEFINITION thaliana genomic Clone SGT751, genomic survey sequence.
ACCESSION BZ666626
VERSION BZ666626.1 GI:28196895
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 494)
Parinov,S., Sevugan,M., De,Y., Yang,W.C., Kumaran,M. and
Sundaresan,V.
Analysis of flanking sequences from dissociation insertion lines: a
database for reverse genetics in Arabidopsis
Plant Cell 11 (12), 2263-2270 (1999)
20057730

PUBMED
COMMENT

10590156
Contact: Sundaresan V
University of California at Davis
Life Sciences Addition 1002, University of California, Davis CA
95616
Email: sundar@ucdavis.edu
This is single pass sequence recovered from the 3' end of the Ds
transposon from the line SGT751. Some insertion lines may have more
than one Ds element, but >90-95% of the lines contain single
insertions. Ds insertions carry a reporter GUS gene as a gene trap.
The line from which the sequence was obtained is available from the
Arabidopsis Biological Resource Center (ABRC), stock number
CS100354. This line can be ordered from the Arabidopsis Information
Resource (TAIR) at <http://arabidopsis.org>
Class: transposon-tagged.

FEATURES
source

Location/Qualifiers
1..494
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Landsberg erecta 0"
/db_xref="taxon:3702"
/clone="SGT751"
/notes="PCR was performed on DNA extracted from five to 15
young seedlings of a given line or from five to 10 young
inflorescences. PCR products were gel-purified and
sequenced to determine the genomic sequence at the site of
insertion."

ORIGIN

Query Match 13.8%; Score 37.4; DB 28; Length 494;
Best Local Similarity 87.2%; Pred. No. 0.58;
Matches 41; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 49 CCGGGTGTGCTACAGGATGAACCGTGGTAACGGTCGGTAA 95
|||||
DB 48 CCGGGAGTGTGATAGGATGAACCGTGGTAACGGTCGGTAA 2
|||||

RESULT 13
CD435731

LOCUS ELOIN0365E01.b Endosperm_3 Zea mays cDNA, mRNA EST 03-JUN-2003
DEFINITION CD435731 650 bp mRNA
ACCESSION CD435731
VERSION CD435731.1 GI:31351374
KEYWORDS EST.

SOURCE
ORGANISM

Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS

Lai, J., Dey, N., Kim, C.S., Becraft, P., Larkins, B., Linton, E. and
Messing, J.

TITLE
JOURNAL

Sequencing of the maize endosperm ESTs
Unpublished (2002)
Contact: Lai, Jinsong
Dr. Joachim Messing's lab
Wakman Institute, Rutgers University
190 Frelinghuysen Rd., Piscataway, NJ 08854, USA
Tel: 732-445-3801
Fax: 732-445-5735
Email: jlai@waksman.rutgers.edu
Seq primer: T3.

FEATURES
source

Location/Qualifiers
1..650
/organism="Zea mays"
/mol_type="mRNA"
/cultivar="W22"
/db_xref="taxon:4577"
/tissue_type="Endosperm of 7-23DAP"
/clone_lib="Endosperm_3"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:

ORIGIN

XhoI"
Query Match 13.8%; Score 37.4; DB 14; Length 650;
Best Local Similarity 74.6%; Pred. No. 0.63;
Matches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 65 AGGATGAAAACGGTCGGTAACGGTAAACGTAACGGAATTTTCCCATCTT 124
|||||
DB 550 AGGATGAAAACGGTCGGTAACGGTAAACGTAACGGAATTTTCCCATCTT 609
|||||
QY 125 TCA 127
DB 610 TAA 612

RESULT 14
CC623062/c

LOCUS OGWHP66TV ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMA0580K12,
DEFINITION CC623062 667 bp DNA linear GSS 19-JUN-2003
ACCESSION CC623062
VERSION CC623062.1 GI:31989483
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE
AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Uterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nurnberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OGWHP66TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: T3
Class: sheared ends.

FEATURES
source

Location/Qualifiers
1..667
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0580K12"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBESK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 13.8%; Score 37.4; DB 29; Length 667;
Best Local Similarity 74.6%; Pred. No. 0.63;
Matches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
QY 65 AGGATGAAAACGGTCGGTAACGGTAAACGTAACGGAATTTTCCCATCTT 124
|||||
DB 284 AGGATGAAAACGGTCGGTAACGGTAAACGTAACGGAATTTTCCCATCTT 225
|||||
QY 125 TCA 127
DB 224 TAA 222

RESULT 15
CC371523/c

LOCUS PUBB230TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTA416F12,
DEFINITION CC371523 837 bp DNA linear GSS 19-MAY-2003

May 17 00:32 17 2004

```
genomic survey sequence.
CC371523
ON CC371523.1 GI:30845140
RDS GSS.
FE Zea mays
ANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 837)
Whitelaw C.A., Quackenbush J., Van Aken S., Utterback T.,
Resnick A., Fraser C.M., Yuan Y., San Miguel P., Ma J. and
Bennetzen J.
Maize Genomics Consortium
Unpublished (2003)
Other GSSs: PUB230TB
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1..837
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA416F12"
/clone_lib="ZM 0.6 1.0 KB"
/note="vector: pCE4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"
IN
try Match 13.8%; Score 37.4; DB 28; Length 837;
at: Local Similarity 74.6%; Pred No. 0.68;
:ches 47; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
65 AGGGATGAAAACGGTCGGTAACGGTCGGTAAATACTACGGGATTTTCCCATCTT 124
795 AGGGATGAAAACGGTCGGTAACGGTCGGTAAATACTACCTTACCGTTTTCATTTTCA 736
125 TCA 127
735 TAA 733
th completed: May 16, 2004, 14:51:44
:ime : 3206 secs
```

This Page Blank (uspio)